

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:51:22 ; Search time 196 Seconds
(without alignments)
672.249 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSLVTL.....IVIGFLGCLCGVSKRSQIV 229

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1215	100.0	229	2 O6UMS1	O6UMS1 homo sapien
2	1215	100.0	229	2 AAO89034	AAG89034 homo sapi
3	1205	99.2	229	2 O9H5X9	O9H5X9 homo sapien
4	924.5	76.1	226	2 O9CQX8	O9CQX8 m mus muscu
5	918.5	75.6	226	2 O9D3Q0	O9D3Q0 mus musculu
6	912.5	75.1	226	2 O9D3R0	O9D3R0 mus musculu
7	182	15.0	197	2 O7SYW6	O7SYW6 xenopus lae
8	173	14.2	197	2 O6FHR6	O6FHR6 homo sapien
9	170	14.0	197	2 O6IB79	O6IB79 homo sapien
10	170	14.0	197	2 AAH69519	AAH69519 homo sapi
11	170	14.0	197	2 CAG33206	CAG33206 homo sapi
12	170	14.0	202	1 T4S1_HUMAN	P30408 homo sapien
13	170	14.0	202	2 CAG33234	CAG33234 homo sapi
14	170	14.0	232	2 O9NE91	O9NE91 homo sapien
15	169	13.9	201	2 O6DHT3	O6DHT3 brachydanio
16	166.5	13.7	202	1 T4S4_HUMAN	AAP36098 homo sapi
17	166.5	13.7	202	1 AAP36098	AAP36098 homo sapi
18	166	13.7	197	1 T4S5_HUMAN	O14894 homo sapien
19	163.5	13.5	198	1 O6DBQ4	O6DBQ4 brachydanio
20	160.5	13.2	202	2 O9EQJ5	O9EQJ5 rattus norv
21	160	13.2	202	1 T4S1_MOUSE	O64302 mus musculu
22	160	13.2	202	2 BAC36752	BAC36752 mus muscu
23	157.5	13.0	202	2 O91XD3	O91XD3 mus musculu
24	151.5	12.5	196	2 O9D8G1	O9D8G1 mus musculu
25	151.5	12.5	196	2 O91XF2	O91XF2 mus musculu
26	141.5	11.6	202	2 O6P8F0	O6P8F0 xenopus tro
27	141.5	11.6	202	2 AAH61278	AAH61278 xenopus t
28	140	11.5	124	2 O9DFD3	O9DFD3 oncorhynch
29	136	11.2	202	1 T4S1_MESAU	P49111 mesocricetu
30	136	11.2	202	2 AAA80343	AAA80343 mesocricetu
31	133	10.9	202	2 O60548	O60548 mesocricetu

32	126	10.4	201	2 O96CE8	O96CE8 homo sapien
33	111.5	9.2	209	2 O96DZ7	O96DZ7 homo sapien
34	103	8.5	1448	2 O8T683	O8T683 dictyosteli
35	101	8.3	450	2 O9D8F3	O9D8F3 m mus muscu
36	100.5	8.3	242	2 O8TNE9	O8TNE9 methanosaer
37	100	8.2	505	2 O89HP9	O89HP9 bradyrhizob
38	99	8.1	351	2 O8CCV8	O8CCV8 mus musculu
39	95.5	7.9	587	2 O86J75	O86J75 dictyosteli
40	94.5	7.8	416	2 O6CTP7	O6CTP7 kluyveromyce
41	94.5	7.8	750	2 O8H4R2	O8H4R2 oryza sativ
42	92	7.6	358	2 O9U2L6	O9U2L6 caenorhabdi
43	91	7.5	365	2 O73LB7	O73LB7 treponema d
44	91	7.5	365	2 AA512462	AA512462 treponema
45	91	7.5	382	2 O8EBW5	O8EBW5 shewanella
46	90.5	7.4	610	1 YFBS_ECOLI	YFBS_ECOLI escherichia
47	90.5	7.4	610	2 O8FF74	O8FF74 escherichia
48	90.5	7.4	1036	2 O7VLE5	O7VLE5 haemophilus
49	90.5	7.4	1044	2 O6LGT2	O6LGT2 photobacter
50	90.5	7.4	1044	2 CAG23498	CAG23498 photobact
51	89.5	7.4	310	2 O9PMF4	O9PMF4 campylobact
52	89	7.3	275	2 O81655	O81655 hemerocalli
53	89	7.3	318	2 O86UG8	O86UG8 homo sapien
54	88.5	7.3	319	2 O76434	O76434 caenorhabdi
55	88.5	7.3	568	2 O9YLE7	O9YLE7 human immun
56	88	7.2	148	2 O65095	O65095 picea maria
57	88	7.2	309	2 O6GJ51	O6GJ51 straphylococ
58	88	7.2	1036	2 O9KV12	O9KV12 vibrio chol
59	87.5	7.2	282	2 O7ZTS1	O7ZTS1 brachydanio
60	87	7.2	470	2 O76BF8	O76BF8 oryzae lat
61	87	7.2	470	2 BAD17898	BAD17898 oryzae 1
62	86.5	7.1	891	2 O9KN09	O9KN09 vibrio chol
63	86	7.1	283	2 O8YSR1	O8YSR1 listeria mo
64	86	7.1	283	2 O71XP0	O71XP0 listeria mo
65	86	7.1	283	2 AAT04925	AAT04925 listeria
66	86	7.1	438	2 O26076	O26076 helicobacte
67	86	7.1	751	2 O8NM62	O8NM62 dictyosteli
68	85.5	7.0	239	2 O9NB10	O9NB10 manduca sex
69	85.5	7.0	271	1 LGT_VIBCH	LGT_VIBCH vibrio chol
70	85.5	7.0	453	1 TDE2_HUMAN	TDE2_HUMAN
71	85	7.0	283	2 O929P6	O929P6
72	85	7.0	328	2 O6PHB1	O6PHB1 brachydanio
73	85	7.0	328	2 AAH56587	AAH56587 brachyd
74	85	7.0	379	1 CYB_PHAAP	CYB_PHAAP
75	85	7.0	379	2 O36471	O36471 phacchoeru
76	85	7.0	557	2 O7XR17	O7XR17 oryza sativ
77	84.5	7.0	156	2 O6S096	O6S096 picea maria
78	84.5	7.0	281	2 O65061	O65061 picea maria
79	84.5	7.0	380	1 CXAL_BRARE	O57474 brachydanio
80	84.5	7.0	381	2 AAQ17183	AAQ17183 brachyd
81	84.5	7.0	381	2 AAO62128	AAG62128 brachyd
82	84.5	7.0	382	2 O73863	O73863 danio aegu
83	84.5	7.0	610	2 O7COP8	O7COP8 shigella fl
84	84.5	7.0	610	2 O83Q63	O83Q63 shigella fl
85	84	6.9	286	2 O824A9	O824A9 salmonella
86	84	6.9	352	1 O9SD_ZOSOP	O9SY9V zosteriasees
87	84	6.9	438	2 O9ZT58	O9ZT58 helicobacte
88	84	6.9	3086	2 O81639	O81639 plasmodium
89	83.5	6.9	142	2 O8H119	O8H119 haliterpis
90	83.5	6.9	331	2 O8KX67	O8KX67 vibrio chol
91	83.5	6.9	560	2 O83DX2	O83DX2 coxiella bu
92	83.5	6.9	752	2 O6LRR1	O6LRR1 photobacter
93	83.5	6.9	752	2 CAG20165	CAG20165 photobact
94	83	6.8	271	1 LGT_VIBVU	LGT_VIBVU vibrio vuln
95	83	6.8	271	1 LGT_VIBVU	LGT_VIBVU vibrio vuln
96	83	6.8	332	2 O76431	O76431 caenorhabdi
97	83	6.8	342	2 O9PT67	O9PT67 xenopus lae
98	83	6.8	451	2 O6BPX5	O6BPX5 campylobact
99	82.5	6.8	138	2 O6X9S5	O6X9S5 allobacilla
100	82.5	6.8	138	2 AAP81930	AAP81930 allobacul
101	82.5	6.8	180	2 O9SPX7	O9SPX7 picea abies
102	82.5	6.8	180	1 PTTG_HUMAN	P33801 homo sapien
103	82.5	6.8	289	2 O9DSU5	O9DSU5 human herpe
104	82.5	6.8	1627	2 O8GU51	O8GU51 oryza sativ

105	82.5	6.8	1628	2	Q7XT6	Q7xt6 oryza sativ	178	80	6.6	379	2	Q9MEF7	Q9mef7 martes amer
106	82	6.7	286	2	Q9XC50	Q9xc50 salmoneia	179	80	6.6	379	2	AAO05992	Aao05992 sus scrof
107	82	6.7	286	2	Q7CPX6	Q7cpX6 salmoneia	180	80	6.6	379	2	AAO06005	Aao06005 sus scrof
108	82	6.7	318	2	Q86UG9	Q86ug9 homo sapien	181	80	6.6	379	2	AAQ06018	Aaq06018 sus scrof
109	82	6.7	379	2	Q85CT9	Q85ct9 sus scrofa	182	80	6.6	379	2	AAQ06044	Aaq06044 sus scrof
110	82	6.7	572	2	Q7XU5	Q7xue5 oryza sativ	183	80	6.6	379	2	AAQ06057	Aaq06057 sus scrof
111	82	6.7	804	2	Q80XB3	Q80xb3 mus musculu	184	80	6.6	379	2	AAQ06070	Aaq06070 sus scrof
112	82	6.7	808	2	Q70W02	Q70w02 ciona intes	185	80	6.6	379	2	AAQ06083	Aaq06083 sus scrof
113	82	6.7	808	2	CAD58841	Cad58841 ciona int	186	80	6.6	379	2	AAQ06096	Aaq06096 sus scrof
114	82	6.7	809	2	Q80XB2	Q80xb2 mus musculu	187	80	6.6	379	2	AAQ06109	Aaq06109 sus scrof
115	82	6.7	823	2	Q80XB6	Q80xb6 mus musculu	188	80	6.6	379	2	AAQ06122	Aaq06122 sus scrof
116	82	6.7	827	2	Q8CDX8	Q8cdx8 mus musculu	189	80	6.6	379	2	AAQ06148	Aaq06148 sus scrof
117	82	6.7	834	2	Q8BH12	Q8bh12 mus musculu	190	80	6.6	379	2	AAQ06161	Aaq06161 sus scrof
118	82	6.7	842	2	Q8R056	Q8r056 mus musculu	191	80	6.6	379	2	AAQ06187	Aaq06187 sus scrof
119	82	6.7	867	1	PML1 MOUSE	Q54990 mus musculu	192	80	6.6	379	2	AAQ06200	Aaq06200 sus scrof
120	82	6.7	976	2	Q6FKX5	Q6fkx5 candida gla	193	80	6.6	379	2	AAQ06213	Aaq06213 sus scrof
121	81.5	6.7	156	2	Q65097	Q65097 picea maria	194	80	6.6	379	2	AAQ06226	Aaq06226 sus scrof
122	81.5	6.7	289	2	P88902	P88902 human herpe	195	80	6.6	379	2	AAQ06239	Aaq06239 sus scrof
123	81.5	6.7	343	2	Q9B4H2	Q9b4h2 cophosaurus	196	80	6.6	406	2	Q6ZC71	Q6zc71 oryza sativ
124	81.5	6.7	347	2	Q6YIV0	Q6yiv0 cophosaurus	197	80	6.6	406	2	BAD09524	Bad09524 oryza sat
125	81.5	6.7	437	2	AAO65533	Aao65533 cophosaur	198	80	6.6	502	2	Q9B973	Q9b973 ceratosolen
126	81.5	6.7	453	2	Q7TNK0	Q7tnk0 rattus norv	199	80	6.6	502	2	Q6BSN4	Q6bsn4 debaryomyce
127	81.5	6.7	454	2	Q8AAS4	Q8aas4 bacteroides	200	80	6.6	502	2	Q8VP06	Q8vp06 bruceia ab
128	81.5	6.7	468	2	Q44515	Q44515 caenorhabdi	201	80	6.6	703	2	Q8VP06	Q8vp06 bruceia ab
129	81.5	6.7	474	2	Q8EP39	Q8ep39 oceanobacil	202	80	6.6	721	2	Q8VG36	Q8vg36 oryza sativ
130	81.5	6.7	672	2	Q6G521	Q6g521 bartonella	203	80	6.6	889	2	Q6ZC72	Q6zc72 oryza sativ
131	81.5	6.7	1019	2	Q83CM1	Q83cm1 coxiella bu	204	80	6.6	889	2	BAD09523	Bad09523 oryza sat
132	81.5	6.7	1040	2	Q87TN1	Q87tn1 vibrio para	205	80	6.6	933	2	Q7R539	Q7r539 giardia lam
133	81.5	6.7	1687	2	Q6O117	Q6o117 rattus norv	206	79.5	6.5	1047	2	Q8EBJ9	Q8ebj9 shewanella
134	81.5	6.7	1687	2	AA566282	Aa666282 rattus no	207	79.5	6.5	154	2	Q9SPW4	Q9spw4 picea glauc
135	81	6.7	150	2	Q9SPX8	Q9spx8 picea abies	208	79.5	6.5	289	2	Q6IUS6	Q6ius6 human herpe
136	81	6.7	254	1	CHIT_PETHY	P29021 pectunia hyb	209	79.5	6.5	341	2	Q8H8B5	Q8hm87 oryza sativ
137	81	6.7	278	2	Q8KEE7	Q8kee7 chlorobium	210	79.5	6.5	356	2	Q8LMZ7	Q8lmz7 oryza sativ
138	81	6.7	318	2	Q86SG9	Q86sg9 homo sapien	211	79.5	6.5	362	2	Q9CNG0	Q9cng0 pasteurella
139	81	6.7	318	2	Q86SH1	Q8esh1 homo sapien	212	79.5	6.5	364	2	Q9L165	Q9l165 arabidopsis
140	81	6.7	318	2	Q86SH3	Q8esh3 homo sapien	213	79.5	6.5	369	2	Q18053	Q18053 caenorhabdi
141	81	6.7	318	2	Q86UG7	Q86ug7 homo sapien	214	79.5	6.5	380	2	Q7N821	Q7n821 photorhabdu
142	81	6.7	379	2	Q85AW1	Q85aw1 sus scrofa	215	79.5	6.5	358	2	Q9M1E2	Q9m1e2 arabidopsis
143	81	6.7	379	2	Q8M707	Q8m707 phacochoru	216	79.5	6.5	608	2	Q8Z523	Q8z523 salmoneia
144	81	6.7	379	2	Q9T568	Q9t568 sus scrofa	217	79.5	6.5	608	2	Q8ZND9	Q8znd9 salmoneia
145	81	6.7	459	2	Q7Y8E6	Q7y8e6 megera wogu	218	79.5	6.5	654	2	Q7TLW5	Q7tlw5 choristoneu
146	81	6.7	461	2	P91197	P91197 caenorhabdi	219	79.5	6.5	654	2	AA2P9812	Aap29812 choristoneu
147	81	6.7	545	2	Q97T02	Q97tj2 clostridium	220	79.5	6.5	662	2	Q83C62	Q83c62 coxiella bu
148	81	6.7	568	2	Q6BYD1	Q6byd1 debaryomyce	221	79	6.5	1143	2	Q9S0B9	Q9s0b9 arabidopsis
149	81	6.7	591	2	Q9J149	Q9j149 rattus norv	222	79	6.5	289	2	Q9Q0G6	Q9q0g6 human herpe
150	81	6.7	622	2	Q9CAV0	Q9cav0 rattus norv	223	79	6.5	379	1	CYB_CEPBA	Q9b5c8 camelus bac
151	81	6.7	703	2	Q8G1T9	Q8g1t9 allulobus	224	79	6.5	379	1	CYB_CEPRI	Q9b5c8 cephalophus
152	81	6.7	748	2	Q44416	Q44416 bruceia su	225	79	6.5	379	1	CYB_CEPRI	Q9b5c1 cephalophus
153	81	6.7	771	2	Q8A9X0	Q8a9x0 bacteroides	226	79	6.5	379	1	CYB_SUSBA	Q8m7c3 sus barbatu
154	81	6.7	1038	2	Q6LVZ3	Q6lvz3 photobacter	227	79	6.5	379	2	Q36543	Q36543 sus barbatu
155	81	6.7	1038	2	CAG18532	Cag18532 photobact	228	79	6.5	379	2	Q6GV99	Q6gv99 sus scrofa
156	81	6.7	4226	2	Q8IH11	Q8ihy1 plasmodium	229	79	6.5	379	2	Q6GV90	Q6gv90 sus scrofa
157	80.5	6.6	205	2	Q6D905	Q6d905 erwinia car	230	79	6.5	379	2	Q6GV91	Q6gv91 sus scrofa
158	80.5	6.6	374	2	Q6RG00	Q6rg00 acinetobact	231	79	6.5	379	2	Q6GV93	Q6gv93 sus scrofa
159	80.5	6.6	379	2	Q9XMB7	Q9xmb7 marimota gal	232	79	6.5	379	2	Q6GV94	Q6gv94 sus scrofa
160	80.5	6.6	395	1	TRFR_CHICK	Q93603 gallus gall	233	79	6.5	379	2	Q8HFA8	Q8hfa8 camelus bac
161	80.5	6.6	838	2	Q8UTC7	Q8utc7 human immu	234	79	6.5	379	2	Q8M702	Q8m7j2 sus barbatu
162	80.5	6.6	878	2	Q8EM47	Q8em47 mycoplasma	235	79	6.5	379	2	Q9B5R9	Q9b5c9 cephalophus
163	80	6.6	140	2	Q85P17	Q85p17 sus scrofa	236	79	6.5	379	2	AAW65581	Aaw65581 camelus b
164	80	6.6	324	2	Q924X8	Q924x8 mus musculu	237	79	6.5	379	2	AAW65581	Aaw65581 camelus b
165	80	6.6	324	2	Q7S346	Q7s346 neuropeptora	238	79	6.5	379	2	AAW65583	Aaw65583 camelus b
166	80	6.6	352	1	Q9PRJ8	Q9ygz2 gobius nige	239	79	6.5	379	2	AAW65584	Aaw65584 camelus b
167	80	6.6	352	2	Q9PRJ8	Q9prj8 xenopus lae	240	79	6.5	379	2	AAW65585	Aaw65585 camelus b
168	80	6.6	356	2	Q9GC80	Q9gc80 pectinomyx s	241	79	6.5	379	2	Q7VFP4	Q7vfp4 hellicobacte
169	80	6.6	356	2	Q9GCS1	Q9gcs1 hylopotes p	242	79	6.5	595	2	Q6YK44	Q6yk44 oryza sativ
170	80	6.6	379	1	CYB_PIG	P24964 sus scrofa	243	79	6.5	595	2	Q84KR4	Q84kr4 oryza sativ
171	80	6.6	379	2	Q7IKJ5	Q7ikj5 sus scrofa	244	79	6.5	595	2	AAW65219	Aaw65219 oryza sat
172	80	6.6	379	2	Q6GV86	Q6gv86 sus scrofa	245	79	6.5	787	2	Q8OV13	Q8ov13 mus musculu
173	80	6.6	379	2	Q85QJ9	Q85qj9 sus scrofa	246	79	6.5	1052	2	Q89FH4	Q89fh4 bradyrhizob
174	80	6.6	379	2	Q9T4J0	Q9t4j0 sus scrofa	247	78.5	6.5	1353	1	CYAA9 MOUSE	P51810 mus musculu
175	80	6.6	379	2	Q9T565	Q9t565 sus scrofa	248	78.5	6.5	208	2	Q7V6B1	Q7v6b1 wolinnella s
176	80	6.6	379	2	Q9T566	Q9t566 sus scrofa	249	78.5	6.5	240	2	Q6P7J5	Q6p7j5 xenopus lae
177	80	6.6	379	2	Q9T567	Q9t567 sus scrofa	250	78.5	6.5	276	2	AAW61648	Aaw61648 xenopus l
												Q9WNS8	Q9wns8 human herpe

251	78.5	6.5	289	2	Q9WHC1	Q9whc1 human herpe	324	77.5	6.4	500	2	O51549	O51549 borrelia bu
252	78.5	6.5	322	2	Q18269	Q18269 caenorhabdi	325	77.5	6.4	557	2	P94622	P94622 clostridium
253	78.5	6.5	328	2	O88775	O88775 rattus norv	326	77.5	6.4	565	2	O8A4R9	O8a4r9 bacteroides
254	78.5	6.5	328	2	AAH61846	Aah61846 rattus no	327	77.5	6.4	825	2	O9FKX1	O9fkx1 arabidopsis
255	78.5	6.5	363	2	Q7CY16	Q7cy16 agrobacteri	328	77.5	6.4	1107	2	Q76NT1	Q76nt1 dictyosteli
256	78.5	6.5	363	2	O8UB66	O8ub66 agrobacteri	329	77.5	6.4	1107	2	AA38831	AA38831 dictyoste
257	78.5	6.5	423	2	O9FH91	Q9fhn1 arabidopsis	330	77	6.3	309	2	O8CTN3	O8ctn3 ethanophylo
258	78.5	6.5	452	2	O8WF40	O8wf40 venerupis (331	77	6.3	314	2	O6ZAX4	O6zax4 oryza sativ
259	78.5	6.5	648	2	Q76L35	Q76l35 nicotiana t	332	77	6.3	314	2	BAC9611	Bac9611 oryza sat
260	78.5	6.5	648	2	BAC23059	Bac23059 nicotiana	333	77	6.3	328	2	O9TR46	O9tr46 platynereis
261	78.5	6.5	760	1	AD25_MOUSE	Q9r159 mus musculu	334	77	6.3	379	2	Q9MNV4	Q9mnv4 martes amer
262	78.5	6.5	1039	2	Q7MQH1	Q7mqh1 vlbrio vuln	335	77	6.3	379	2	Q9B5Q9	Q9b5q9 cephalopus
263	78.5	6.5	1039	2	Q8DDC6	Q8ddc6 vlbrio vuln	336	77	6.3	379	2	O9G4V1	O9g4v1 martes amer
264	78	6.4	227	2	Q74HY8	Q74hy8 lactobacilli	337	77	6.3	379	2	O9G7S6	O9g7s6 sus scrofa
265	78	6.4	227	2	AA509552	AA509552 lactobaci	338	77	6.3	379	2	O8WBM1	O8wbm1 martes amer
266	78	6.4	285	2	O92L13	Q92l13 rhizobium m	339	77	6.3	424	2	O6D8S9	O6d8s9 erwina car
267	78	6.4	297	2	O8NXT3	Q8nxt3 ethaphylococ	340	77	6.3	452	2	O6BQ77	O6bq77 debaryomyce
268	78	6.4	309	2	O6GBL1	O6gbl1 ethaphylococ	341	77	6.3	471	2	O85YML	O85ym1 monadenium
269	78	6.4	309	2	O99VZ6	O99vz6 ethaphylococ	342	77	6.3	516	2	O9B5Z5	O9b5z5 pseudoselylo
270	78	6.4	309	2	Q7A731	Q7a731 ethaphylococ	343	77	6.3	534	2	O8RWH6	O8rwh6 arabidopsis
271	78	6.4	329	2	Q76BK6	Q76bk6 paraliichthy	344	77	6.3	537	2	O7S496	O7s496 neurospora
272	78	6.4	329	2	BAD02483	Bad02483 paraliichth	345	77	6.3	577	2	O85Q07	O85q07 gomphioceph
273	78	6.4	356	2	O8WF83	Q8wf83 petaurista	346	77	6.3	581	1	PLRL_SHEEP	PLrl_sheep ovis aries
274	78	6.4	379	1	CYB_CEPHR	Q9tld4 cephalorhyn	347	77	6.3	590	2	Q9STC7	Q9stc7 dunaliella
275	78	6.4	379	1	CYB_PHAAR	O8m708 phacochoeiru	348	77	6.3	677	2	Q7OS58	Q7os58 giardia lam
276	78	6.4	379	2	O8M709	O8m709 phacochoeiru	349	77	6.3	1032	1	X995_HAEIN	X995124 haemophilus
277	78	6.4	379	2	O9XMC0	O9xmc0 marmota cau	350	77	6.3	1061	2	O986H1	O986h1 rhizobium l
278	78	6.4	379	2	Q92L18	Q92l18 rhizobium m	351	77	6.3	1188	2	Q7RMN3	Q7rmn3 neurospora
279	78	6.4	380	2	Q7Y752	Q7y752 zoogoneticu	352	77	6.3	1215	2	P937S0	P937s0 arabidopsis
280	78	6.4	380	2	Q7YHK2	Q7yhk2 zoogoneticu	353	77	6.3	2651	2	O81AV6	O81av6 plasmodium
281	78	6.4	409	2	Q73GC5	Q73gc5 wolbachia p	354	77	6.3	222	2	Q7B5K3	Q7b5k3 lactobacilli
282	78	6.4	409	2	AA514691	AA514691 wolbachia	355	76.5	6.3	222	2	AA521881	AA521881 lactobacci
283	78	6.4	457	2	O8A565	O8a565 bacteroides	356	76.5	6.3	232	2	O6MGS9	O6mgs9 rattus norv
284	78	6.4	519	2	O6CXK7	O6cxk7 khuyetomye	357	76.5	6.3	232	2	CAB83987	Ceb83987 rattus no
285	78	6.4	555	2	O869R1	O869r1 dictyosteli	358	76.5	6.3	248	2	Q7QIX9	Q7qix9 giardia lam
286	78	6.4	641	2	Q7Z2W2	Q7z2w2 paraliichthy	359	76.5	6.3	268	2	O6XFA1	O6xf1 psammophis
287	78	6.4	717	2	Q7XKFA	Q7xkfa oryza sativ	360	76.5	6.3	268	2	AA78955	AAp78955 psammophi
288	78	6.4	832	2	O8IBR8	O8ib8 plasmodium	361	76.5	6.3	274	2	O995B5	O995b5 human herpe
289	78	6.4	989	2	O6FPA6	O6fpa6 candida gla	362	76.5	6.3	289	2	O80ID9	O80id9 human herpe
290	78	6.4	1059	2	O88HD4	Q88hd4 pseudomonas	363	76.5	6.3	289	2	O80IF2	O80if2 human herpe
291	78	6.4	1062	2	P95422	P95422 pseudomonas	364	76.5	6.3	333	2	O8KXV0	O8kxv0 human herpe
292	78	6.4	1062	2	Q91OY8	Q91oy8 pseudomonas	365	76.5	6.3	343	2	O859X2	O859x2 una exsul.
293	78	6.4	1280	2	O86JUR7	O86jur7 dictyosteli	366	76.5	6.3	343	2	O85KP0	O85kp0 una exsul.
294	78	6.4	1783	2	O18698	O18698 caenorhabdi	367	76.5	6.3	377	2	O8KOP5	O8kop5 mus musculu
295	78	6.4	1877	2	O8MCA1	O8mca1 caenorhabdi	368	76.5	6.3	379	1	CYB_CANRA	Cyb_canra canis fami
296	77.5	6.4	151	2	O9SPX9	Q9spk9 picea abies	369	76.5	6.3	379	1	CYB_MARKR	Cyb_marck marmota mar
297	77.5	6.4	218	2	O932K2	Q932k2 ethaphylococ	370	76.5	6.3	379	1	CYB_MARVA	Cyb_marva marmota van
298	77.5	6.4	274	2	O995A5	O995a5 human herpe	371	76.5	6.3	379	2	O6JWX5	O6jwx5 canis aureu
299	77.5	6.4	320	2	O6D431	O6d431 erwina car	372	76.5	6.3	379	2	O6JWX7	O6jwx7 canis aureu
300	77.5	6.4	343	2	O9BAH0	Q9bah0 callisaurus	373	76.5	6.3	379	2	O6Y8J2	O6y8j2 canis lupus
301	77.5	6.4	347	2	O6YTUS	O6ytus callisaurus	374	76.5	6.3	379	2	O9G3W7	O9g3w7 rhizomys si
302	77.5	6.4	347	2	AAO65538	AAo65538 callisaur	375	76.5	6.3	379	2	BAB35140	Bab35140 canis fam
303	77.5	6.4	379	1	CYB_LAMVI	Q963227 lama vicugn	376	76.5	6.3	379	2	AAAN85622	AAan85622 canis lup
304	77.5	6.4	379	1	Q9TR33	Q9tr33 marmota cau	377	76.5	6.3	379	2	AAQ56601	AAq56601 canis lup
305	77.5	6.4	379	2	O9TFP4	O9tfp4 spermophilu	378	76.5	6.3	379	2	AAQ56603	AAq56603 canis aur
306	77.5	6.4	379	2	O9TP95	Q9tp95 spermophilu	379	76.5	6.3	426	2	O9W3P5	O9w3p5 drosophila
307	77.5	6.4	379	2	O8M9B4	Q8m9b4 sciturus aes	380	76.5	6.3	451	2	O69657	O69657 mycobacteri
308	77.5	6.4	434	2	O6NF28	O6nf28 corynebacte	381	76.5	6.3	451	2	O7TVX6	O7tvx6 mycobacteri
309	77.5	6.4	434	2	CAE50266	CAe50266 corynebac	382	76.5	6.3	538	2	O9MLT4	Q9mlt4 arabidopsis
310	77.5	6.4	437	2	Q7WR18	Q7wr18 ethaphylococ	383	76.5	6.3	556	2	O6BVD3	O6bvd3 debaryomyce
311	77.5	6.4	452	2	O7YFA5	O7yfa5 venerupis (384	76.5	6.3	557	2	O6FLC9	O6flc9 candida gla
312	77.5	6.4	452	2	O7YPA7	Q7yfa7 venerupis (385	76.5	6.3	557	2	Q7KVUS	Q7kvus drosophila
313	77.5	6.4	452	2	Q7YF50	Q7yfe50 venerupis (386	76.5	6.3	557	2	AA656269	AA656269 drosophila
314	77.5	6.4	452	2	Q7YF51	Q7yfe51 venerupis (387	76.5	6.3	574	2	O9TW13	Q9tw13 leishmania
315	77.5	6.4	452	2	Q7YF52	Q7yfe52 venerupis (388	76.5	6.3	594	2	O9UIG0	Q9ui90 leishmania
316	77.5	6.4	453	1	TDE2_MOUSE	Q9qz18 mus musculu	389	76.5	6.3	614	1	DNAK_ODOSI	DNak_odosi onchocerca
317	77.5	6.4	456	1	O6BQ78	O6bq78 debaryomyce	390	76.5	6.3	722	2	O9FOW5	O9fow5 pseudomonas
318	77.5	6.4	459	1	NT4M_RABIT	O79436 cyccolagus	391	76	6.3	141	2	O47929	O47929 exonema tr
319	77.5	6.4	459	2	O6CQC4	O6cqc4 ethaphylococ	392	76	6.3	249	2	O7R5F7	O7r5f7 giardia lam
320	77.5	6.4	459	2	O6GK34	O6gk34 ethaphylococ	393	76	6.3	289	1	O8D5C4	O8d5c4 comophorus
321	77.5	6.4	459	2	O99X01	O99x01 ethaphylococ	394	76	6.3	310	2	O8TVG9	O8tv94 mus musculu
322	77.5	6.4	459	2	Q7AIX0	Q7aix0 ethaphylococ	395	76	6.3	312	2	O8TVG9	O8tv94 mus musculu
323	77.5	6.4	494	2	O87S84	O87s84 vibrio para	396	76	6.3	330	2	O85T18	O85t18 anolis roqu

397	76	6.3	343	2	Q85KP4	Q85kp4 uma exsul.	470	75.5	6.2	409	1	MNTH_YERPE	Q8zc12 yerinia pe
398	76	6.3	346	2	O16913	O16913 caenorhabdi	471	75.5	6.2	431	2	Q9S333	Q9s333 prochloroco
399	76	6.3	379	1	CYB_MARME	Cyct39 mares mela	472	75.5	6.2	431	2	Q7BW18	Q7bw.8 prochloroco
400	76	6.3	379	1	CYB_PTEHP	O8sf24 pterocof hy	473	75.5	6.2	476	2	Q9S1A5	Q9s1a5 aradiopsis
401	76	6.3	379	2	O787Z6	O787z6 scrofa	474	75.5	6.2	494	2	Q7NMN2	Q7nmn2 vibrio vuln
402	76	6.3	379	2	O711Z0	Q711z0 mares zibe	475	75.5	6.2	494	2	Q8DEP3	Q8dep3 vibrio vuln
403	76	6.3	379	2	Q8M700	Q8m700 mares zibe	476	75.5	6.2	578	2	Q8SUI2	Q8su.i2 ciona savig
404	76	6.3	379	2	Q8M701	Q8m701 sus verruco	477	75.5	6.2	593	2	Q6EM61	Q6em61 debaryomyce
405	76	6.3	379	2	Q9T7P0	Q9t7p0 tachyrycte	478	75.5	6.2	609	2	Q8ERZ5	Q8erz5 pseudomonas
406	76	6.3	379	2	Q9BSR7	Q9bsr7 cephalophus	479	75.5	6.2	788	1	Q0XM_SULAC	P39481 sulfolobus
407	76	6.3	379	2	Q9GBH0	Q9gbh0 mares mart	480	75.5	6.2	824	2	O40713	O407.3 oryza sativ
408	76	6.3	379	2	Q9GBH3	Q9gbh3 mares amer	481	75.5	6.2	849	2	Q8T3V2	Q8t3v2 drosophila
409	76	6.3	379	2	Q8W7D6	Q8w7d6 mares mart	482	75.5	6.2	864	2	Q6BCY9	Q6bcy9 debaryomyce
410	76	6.3	379	2	Q8WBW0	Q8wbw0 mares zibe	483	75.5	6.2	886	2	Q8KAY9	Q8kay9 chlorobium
411	76	6.3	380	2	O7YE34	O7ye34 microspatho	484	75.5	6.2	1099	2	O18633	O186.3 caenorhabdi
412	76	6.3	380	2	O7YHK3	O7yhk3 zoogoneticu	485	75.5	6.2	1099	2	CAA9786	CAa9786 caenorhab
413	76	6.3	405	2	O6L2S9	O6l2s9 picrophilus	486	75.5	6.2	1173	2	AAQ23543	AAq23543 drosophila
414	76	6.3	410	2	Q9XP09	Q9xp09 parapanetele	487	75.5	6.2	1173	2	AAQ23543	AAq23543 drosophila
415	76	6.3	430	2	O6Y0P9	O6y0p9 staphylococ	488	75.5	6.2	1683	2	Q8KRT1	Q8krt1 dictyostell
416	76	6.3	430	2	AAp32320	AAp32320 staphyloc	489	75.5	6.2	1683	2	AAO50849	AAo50849 dictyoste
417	76	6.3	431	2	O6LWQ4	O6lwq4 lactobacill	490	75.5	6.2	4226	2	Q9N9H5	Q9n9h5 plasmodium
418	76	6.3	431	2	O8Y7H9	O8y7h9 listeria mo	491	75	6.2	111	2	Q9XEP7	Q9xe7 aradiopsis
419	76	6.3	431	2	CAG17844	Cag17844 lactobaci	492	75	6.2	176	2	O8T1K1	O8t1k1 methanosarc
420	76	6.3	445	2	Q76L72	Q76l72 euphausia s	493	75	6.2	253	2	Q8AMJ8	Q8amj8 chlorosocob
421	76	6.3	445	2	BAD16768	Bad16768 euphausia	494	75	6.2	289	2	Q8AMR5	Q8amr5 brachydanio
422	76	6.3	447	2	O6G7B5	O6g7b5 staphylococ	495	75	6.2	312	2	Q6MPX2	Q6mtx2 rattus norv
423	76	6.3	447	2	O8VU55	O8vu55 staphylococ	496	75	6.2	312	2	CAE84075	CAe84075 rattus no
424	76	6.3	447	2	O8NV80	O8nv80 staphylococ	497	75	6.2	330	2	O8S7I5	O8sc.5 anolis roqu
425	76	6.3	447	2	O9NS97	O9ns97 staphylococ	498	75	6.2	330	2	O8S7I6	O8sc.6 anolis roqu
426	76	6.3	453	2	Q6UKF6	Q6ukf6 phoronis ps	499	75	6.2	347	2	O6Y1W1	O6y1w1 phrynosoma
427	76	6.3	453	2	AAr13394	AAr13394 phoronis	500	75	6.2	347	2	AAO65522	AAo65522 phrynosom
428	76	6.3	505	2	Q972X7	Q972x7 sulfolobus	501	75	6.2	360	2	Q8HIC0	Q8hic0 callosciuru
429	76	6.3	515	2	O8BG43	O8bg43 m mus muscu	502	75	6.2	373	2	Q8Z0B9	Q8z0b9 anabaena sp
430	76	6.3	515	2	O8C8L1	O8c8l1 mus musculu	503	75	6.2	379	1	CYB_CEPNG	Q9b5r0 cephalophus
431	76	6.3	528	1	O8OU08	O8ou08 mus musculu	504	75	6.2	379	1	CYB_GIKGU	P56677 guilo guilo (
432	76	6.3	532	1	YHCA_BACSU	Yhca bacsu	505	75	6.2	379	1	CYB_MESHI	Q35000 mesomya his
433	76	6.3	559	2	Q7QR36	Q7qr36 giardia lam	506	75	6.2	379	2	O9J341	O9j341 aepeyceros m
434	76	6.3	559	2	O7QR36	O7qr36 giardia lam	507	75	6.2	379	2	P92879	P925r9 bubalus dep
435	76	6.3	561	2	O17947	O17947 caenorhabdi	508	75	6.2	379	2	P92867	P928r7 bubalus dep
436	76	6.3	604	2	O93700	O93700 sulfolobus	509	75	6.2	379	2	O7G1O4	O7g1o4 mesomya his
437	76	6.3	742	2	O23766	O23766 chironomus	510	75	6.2	379	2	O7IYN8	O7iyn8 cephalophus
438	76	6.3	751	2	O01835	O01835 caenorhabdi	511	75	6.2	379	2	O8HBR1	O8hb.r1 camelus bac
439	76	6.3	814	2	Q9VNP2	Q9vnp2 drosophila	512	75	6.2	379	2	O8HFA7	O8hfa7 camelus bac
440	76	6.3	814	2	AAf51887	AAf51887 drosophila	513	75	6.2	379	2	Q9XK52	Q9xk52 marmota sib
441	76	6.3	981	2	Q7Q074	Q7q074 anopheles g	514	75	6.2	379	2	Q9XLD8	Q9xld8 kobus ellip
442	76	6.3	1011	2	O24273	O24273 drosophila	515	75	6.2	379	2	O9XLD9	O9xld9 kobus ellip
443	76	6.3	1043	2	O6LNM7	O6lnm7 photobacter	516	75	6.2	379	2	O9B1D2	O9b1d2 cephalophus
444	76	6.3	111	2	Q90X36	Q90x36 photobact	517	75	6.2	379	2	Q9B5Q3	Q9b5q3 cephalophus
445	76	6.2	138	2	P71459	P71459 lactobacill	518	75	6.2	379	2	Q9BSR6	Q9bs.r6 cephalophus
446	75.5	6.2	142	2	O8HWM9	O8hwm9 allodape mu	519	75	6.2	380	2	O7YE73	O7yer73 chromis xan
447	75.5	6.2	151	2	O8SPW5	O8spw5 picea glauc	520	75	6.2	380	2	O9T578	O9t578 acomya sp.
448	75.5	6.2	222	2	O88ZC6	O88zc6 lactobacill	521	75	6.2	385	2	O9PFR8	O9pfr8 xylella fas
449	75.5	6.2	239	2	O75OB4	O75qb4 human coxsa	522	75	6.2	385	2	O8DZQ7	O8dzq7 wiggleswort
450	75.5	6.2	239	2	O6DCQ3	O6dcq3 xenopus lae	523	75	6.2	385	2	O8DZQ7	O8dzq7 wiggleswort
451	75.5	6.2	239	2	BAD11163	Bad11163 human cox	524	75	6.2	452	2	Q6GMG6	Q6gm6 brachydanio
452	75.5	6.2	239	2	O6G1G5	O6g1g5 staphylococ	525	75	6.2	519	2	O6R196	O6r196 rhizobium f
453	75.5	6.2	275	2	O6G1G5	O6g1g5 staphylococ	526	75	6.2	519	2	AAr1685	AAr1685 rhizobium
454	75.5	6.2	343	2	O85C80	O85c80 una exsul.	527	75	6.2	527	2	O8KJ76	O8kj76 enterococcu
455	75.5	6.2	343	2	O85KPI	O85kpi una exsul.	528	75	6.2	566	2	Q73YMO	Q73ym0 mycobacteri
456	75.5	6.2	347	2	O6Y1U9	O6y1u9 holbrookia	529	75	6.2	566	2	AAO4252	AAo4252 mycobacte
457	75.5	6.2	347	2	AAO65534	AAo65534 holbrooki	530	75	6.2	570	2	Q9B510	Q9b510 tetrodonpoc
458	75.5	6.2	348	2	O8MOU1	O8mou1 paracentrot	531	75	6.2	581	1	PRLR_BOVIN	Q28172 bos taurus
459	75.5	6.2	364	2	O92PR2	O92pr2 rhizobium m	532	75	6.2	726	2	O6C7B9	O6c7b9 yarrowia li
460	75.5	6.2	378	2	Q7OEH3	Q7oeh3 saccosomus	533	75	6.2	853	2	O93245	O93245 oncorhynch
461	75.5	6.2	378	2	CAE48144	CAe48144 saccosom	534	75	6.2	1015	2	O09938	O09938 caenorhabdi
462	75.5	6.2	379	2	O20611	O20611 coetomys da	535	75	6.2	2201	1	TEHA_HUMAN	P24831 homo sapien
463	75.5	6.2	379	2	O21789	O21789 ctenomys fir	536	74.5	6.1	146	2	Q8LXC1	Q8lxc1 mares amer
464	75.5	6.2	379	2	O6T8R4	O6t8r4 spermophilu	537	74.5	6.1	202	2	Q6ZV01	Q6zv01 homo sapien
465	75.5	6.2	379	2	O9XP28	O9xp28 marmota cal	538	74.5	6.1	202	2	BAC86065	Bac85065 mus sapi
466	75.5	6.2	379	2	Q9GBG7	Q9gbg7 guilo guilo (539	74.5	6.1	239	2	O8BJU2	O8bjj2 mus musculu
467	75.5	6.2	379	2	AAr88275	AAr88275 spermophi	540	74.5	6.1	246	2	Q9MR63	Q9mf.3 beta vulgar
468	75.5	6.2	380	2	O94SX5	O94sx5 cololabie s	541	74.5	6.1	265	2	O896Z5	O896z5 clostridium
469	75.5	6.2	384	2	Q37623	Q37623 prototheca	542	74.5	6.1	268	2	O6N1Z8	O6n1z8 corynebacte

1419	70	5.8	379	2	AAR88320	Aar88320 spectromphi
1420	70	5.8	379	2	AAP42537	AAP42537 proechimy
1421	70	5.8	379	2	AAP42538	AAP42538 proechimy
1422	70	5.8	379	2	AAP42539	AAP42539 proechimy
1423	70	5.8	379	2	AAP42540	AAP42540 proechimy
1424	70	5.8	379	2	AAP42541	AAP42541 proechimy
1425	70	5.8	379	2	AAP42542	AAP42542 proechimy
1426	70	5.8	379	2	AAP42543	AAP42543 proechimy
1427	70	5.8	379	2	AAP42544	AAP42544 proechimy
1428	70	5.8	379	2	AAP42545	AAP42545 proechimy
1429	70	5.8	379	2	AAP42546	AAP42546 proechimy
1430	70	5.8	379	2	AAP42547	AAP42547 proechimy
1431	70	5.8	379	2	AAQ08020	AAQ08020 vixericu
1432	70	5.8	379	2	AAQ08021	AAQ08021 vixericu
1433	70	5.8	380	2	O7YHK0	O7YHK0 zoogoneticu
1434	70	5.8	380	2	O8HNM9	O8HNM9 myomys dero
1435	70	5.8	381	2	O7YCT7	O7YCT7 apomy's grac
1436	70	5.8	398	1	TRFR_SHEEP	O28596 ov's aries
1437	70	5.8	429	1	ARSB_STRAW	O8HW09 staphylococ
1438	70	5.8	430	2	O6YOB6	O6YOB6 staphylococ
1439	70	5.8	430	2	AAP32323	AAP32323 staphyloc
1440	70	5.8	432	2	O8BNQ4	O8BNQ4 oceanobacil
1441	70	5.8	435	2	O6G2S6	O6G2S6 bartoneila
1442	70	5.8	437	2	O8PRW9	O8PRW9 methanosarc
1443	70	5.8	437	2	O64811	O64811 arabidopsis
1444	70	5.8	438	1	CLN3_CANPA	O29611 canis famli
1445	70	5.8	459	2	O9G3F4	O9G3F4 chalinolobu
1446	70	5.8	482	2	O6T3V7	O6T3V7 halomonas e
1447	70	5.8	482	2	AAR91792	AAR91792 halomonas
1448	70	5.8	484	2	O73RS3	O73RS3 treponema d
1449	70	5.8	484	2	AAS10510	AAS10510 treponema
1450	70	5.8	485	2	O86HV0	O86HV0 dictyosteli
1451	70	5.8	485	2	O8NQC2	O8NQC2 corynebacte
1452	70	5.8	490	1	MOT3_YEAST	PS4785 asccaromyc
1453	70	5.8	494	2	O8EVI8	O8EVI8 mycoplasma
1454	70	5.8	503	2	O8L6Z8	O8L6Z8 arabidopsis
1455	70	5.8	503	2	AAQ56818	AAQ56818 arabidops
1456	70	5.8	505	2	O6MSA9	O6MSA9 corynebacte
1457	70	5.8	505	2	CAF21482	CAF21482 corynebac
1458	70	5.8	507	2	O9CMF8	O9CMF8 pasteurella
1459	70	5.8	510	1	ABGT_ECOLI	P46133 escherichia
1460	70	5.8	512	2	O9JUN6	O9JUN6 nisseeria m
1461	70	5.8	514	2	O9CPB6	O9CPB6 pasteurella
1462	70	5.8	520	2	O9SHJ2	O9SHJ2 arabidopsis
1463	70	5.8	542	2	O5S340	O5S340 avian infec
1464	70	5.8	557	2	O9M1E1	O9M1E1 arabidopsis
1465	70	5.8	559	2	O8SRA2	O8SRA2 encephalito
1466	70	5.8	578	1	TRM1_DROME	O18257 caenorhabdi
1467	70	5.8	581	2	O18257	O18257 caenorhabdi
1468	70	5.8	581	2	CAB16542	CAB16542 caenorhab
1469	70	5.8	607	2	O6Y4R2	O6Y4R2 cucumaria m
1470	70	5.8	607	2	AAR02393	AAR02393 cucumaria
1471	70	5.8	668	2	O9BR66	O9BR66 homo sapien
1472	70	5.8	689	2	O7JMO5	O7JMO5 caenorhabdi
1473	70	5.8	689	2	CAB48501	CAB48501 caenorhab
1474	70	5.8	710	2	O23383	O23383 arabidopsis
1475	70	5.8	733	2	O6BR14	O6BR14 debaratomyce
1476	70	5.8	745	2	O19870	O19870 caenorhabdi
1477	70	5.8	745	2	CAA92675	CAA92675 caenorhab
1478	70	5.8	800	2	O6BJU9	O6BJU9 debaratomyce
1479	70	5.8	841	2	O6KZG3	O6KZG3 plicrophilus
1480	70	5.8	853	2	O7RWS6	O7RWS6 neurospora
1481	70	5.8	857	2	O733S1	O733S1 human immun
1482	70	5.8	860	2	O998B5	O998B5 human immun
1483	70	5.8	860	2	O998B5	O998B5 human immun
1484	70	5.8	1034	2	O8PQ66	O8PQ66 xanthomonas
1485	70	5.8	1091	1	RHG7_RAT	O63744 r rho-gcpas
1486	70	5.8	1097	1	O8T2F8	O8T2F8 dictyosteli
1487	70	5.8	1748	1	POLR_EIV	P35928 erysimum la
1488	70	5.8	1748	1	AAC80555	AAC80555 erysimum
1489	70	5.8	2049	2	O25150	O25150 halocynthia
1490	70	5.8	4060	2	O9IH28	O9IH28 gill-associ
1491	69.5	5.7	142	2	O8HIP9	O8HIP9 brevinaire

1492	69.5	5.7	158	2	O9ZLA6	O9ZLA6 helicobacte
1493	69.5	5.7	193	2	O6M6S5	O6M6S5 canis famli
1494	69.5	5.7	193	2	AAQ95550	AAQ95550 canis fam
1495	69.5	5.7	210	2	O81546	O81546 plasmodium
1496	69.5	5.7	210	2	O7381L	O7381L bacillus ce
1497	69.5	5.7	210	2	AAS41301	AAS41301 bacillus
1498	69.5	5.7	231	2	O8ZSC7	O8ZSC7 anabaena ap
1499	69.5	5.7	243	2	O8WEL6	O8WEL6 pogonomyrme
1500	69.5	5.7	255	2	O86BW2	O86BW2 drosophila

ALIGNMENTS

RESULT 1

ID	O6UMS1	PRELIMINARY;	PRT;	229 AA.
AC	O6UMS1;			
DT	05-JUL-2004 (TREMblrel. 27, Created)			
DT	05-JUL-2004 (TREMblrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMblrel. 27, Last annotation update)			
DE	TCCE518.			
GN	ORFNames=UNQ518;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2287296; PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,			
RA	Eaton D., Foster J., Gilmaldi L., Gu Q., Hesse P.E., Heldeus S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark W., Robbie B., Sanchez C., Schoenfeld J.,			
RA	Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.,			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL: AY358671; AAQ89034.1; --			
DR	InterPro: IPR008661; L6_membrane.			
DR	Pfam: PF05805; L6_membrane; 1.			
DR	SEQUENCE 229 AA; 25109 MW; 1718BD342C58C903 CRC64;			
Query Match	100.0%; Score 1215; DB 2; Length 229;			
Best Local Similarity	100.0%; Pred. No. 3.2e-99;			
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEDDQFSQNPISCFEWMFPGIIGAGL	60	
DB	1	MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEDDQFSQNPISCFEWMFPGIIGAGL	60	
QY	61	MAIPATWISLTARRACCNRTGWFSSFPSTVIVIGALYCMILISQALLKGPLMCNPS	120	
DB	61	MAIPATWISLTARRACCNRTGWFSSFPSTVIVIGALYCMILISQALLKGPLMCNPS	120	
QY	121	NSNANCFESLKNISDIHPESFNLOMFNDSCAPPTGKFNKPTSNNTMASGMRASSFHFPS	180	
DB	121	NSNANCFESLKNISDIHPESFNLOMFNDSCAPPTGKFNKPTSNNTMASGMRASSFHFPS	180	
QY	181	ENKRLIHFSVFGLLVLVGLILEVLFGLSQIVIGFGLCGVSKRRSQIV	229	
DB	181	ENKRLIHFSVFGLLVLVGLILEVLFGLSQIVIGFGLCGVSKRRSQIV	229	
RESULT 2				
AAQ89034	PRELIMINARY;	PRT;	229 AA.	
AAQ89034;				

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DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE TCCE518.
GN UNQ518.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurey A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
RA Seeborg S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358671; AAC09034.1; -
SQ SEQUENCE 229 AA; 25109 MW; 1718ED34258C903 CRC64;

Query Match 100.0%; Score 1215; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.2e-99;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCCEGWTSCNGFSLVLLLVGVNNAIPLIYSLVEEDQFSONPISCFEWWFPGIIGAGL 60
DB 1 MTCCEGWTSCNGFSLVLLLVGVNNAIPLIYSLVEEDQFSONPISCFEWWFPGIIGAGL 60
QY 61 MAIPATMTSLTARKRACCCNRTGMFLSFFSVITVIGALYCMILISQALLKPIIMCNSPS 120
DB 61 MAIPATMTSLTARKRACCCNRTGMFLSFFSVITVIGALYCMILISQALLKPIIMCNSPS 120
QY 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
DB 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
QY 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
DB 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
QY 181 ENKRLIHFSVFLGLLVGLVLEVLFGLSQIVIGFGLGCLGVSKRSQIV 229
DB 181 ENKRLIHFSVFLGLLVGLVLEVLFGLSQIVIGFGLGCLGVSKRSQIV 229

RESULT 3
Q9H5X9 PRELIMINARY; PRT; 229 AA.
AC Q9H5X9;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ22800.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ileal mucosa;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Oca T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isegaki T., Sugano S.;
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK026453; BAB15488.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.

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DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 229 AA; 25103 MW; B7505D2798B34CDF CRC64;

Query Match 99.2%; Score 1205; DB 2; Length 229;
Best Local Similarity 99.1%; Pred. No. 2.5e-98;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTCCEGWTSCNGFSLVLLLVGVNNAIPLIYSLVEEDQFSONPISCFEWWFPGIIGAGL 60
DB 1 MTCCEGWTSCNGFSLVLLLVGVNNAIPLIYSLVEEDQFSONPISCFEWWFPGIIGAGL 60
QY 61 MAIPATMTSLTARKRACCCNRTGMFLSFFSVITVIGALYCMILISQALLKPIIMCNSPS 120
DB 61 MAIPATMTSLTARKRACCCNRTGMFLSFFSVITVIGALYCMILISQALLKPIIMCNSPS 120
QY 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
DB 121 NSNANCEFSLKNSIDIHPSFNLQWPFNDSCAPPTGFKPTSDTMAWGKRASSFHFDSE 180
QY 181 ENKRLIHFSVFLGLLVGLVLEVLFGLSQIVIGFGLGCLGVSKRSQIV 229
DB 181 ENKRLIHFSVFLGLLVGLVLEVLFGLSQIVIGFGLGCLGVSKRSQIV 229

RESULT 4
Q9COY8 PRELIMINARY; PRT; 226 AA.
AC Q9COY8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA.
DE RIKEN full-length enriched library, clone:503346G15 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI2630 (Mus musculus 10 day old male
DE pancreas cDNA, RIKEN full-length enriched library, clone:1610018H02
DE product:similar to cDNA: FLJ22800 FIS, CLONE KAI2630).
GN Name=1810018L02R1K;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and pancreas;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komoto H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaka S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and pancreas;
 RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Komoto H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN EMBL; AK017195; BAB30629.1;
 DR EMBL; AK007532; BAB25093.1;
 DR MGD; MGI:1913511; 1810018L02R1K.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR008661; L6_membrane.
 DR Pfam; PF05805; L6_membrane; 1.
 SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA16CA335EAD CRC64;
 Query Match 76.1%; Score 924.5; DB 2; Length 226;
 Best Local Similarity 74.2%; Pred. No. 1.4e-73;
 Matches 170; Conservative 27; Mismatches 29; Indels 3; Gaps 2;
 QY 1 MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEEDQFSQNPISCFEWMFPGIIGAGL 60
 DB 1 MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEEDQFSQNPISCFEWMFPGIIGAGL 60
 QY 61 MATPATMTSLTARRACCNRTGWFSLSPSVITVIGALYCMILISQALLKGPIMCMSPS 120
 DB 61 MATPATMTSLAARRRACCNRTGWFSLSPSVITVIGAVYCMVLSQALLKGPIMCMSPS 120
 QY 121 NSNANCFSLKNTSIDIPESFNLOMPFNDSCAPPTGKPKPTSDNTMASGWRASFFHPDSE 180
 DB 121 NSVTTCFSLKNTSKPDESFNLMFNGTCVSTPTDKRPPIIN-MSNWKIP--NSNSE 177
 QY 181 ENKRRLHFSVFLGLLVGLLEVLFGLSQIVTIGFGLCGVSKRRSQIV 229
 DB 178 EDRHRIRHFSVFMVLLVGLLEVLFGLSQIVTIGFGLCGVSKRRSQIV 226
 RESULT 5
 Q9D3Q0 PRELIMINARY; PRT; 226 AA.
 AC Q9D3Q0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033430P14 product:similar
 DE to CDNA: FLJ22800 FIS, CLONE KAI2630.
 GN Name=1810018L02R1K;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RL "High-efficiency full-length cDNA cloning.";
 RM Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA The FANTOM Consortium;
 RL "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komoto H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaka S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Komoto H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN EMBL; AK017209; BAB30635.1;
 DR MGD; MGI:1913511; 1810018L02R1K.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR008661; L6_membrane.
 DR Pfam; PF05805; L6_membrane; 1.
 SQ SEQUENCE 226 AA; 24786 MW; 3FE6BA06703344B7 CRC64;
 Query Match 75.6%; Score 918.5; DB 2; Length 226;
 Best Local Similarity 73.8%; Pred. No. 4.9e-73;
 Matches 165; Conservative 27; Mismatches 30; Indels 3; Gaps 2;
 QY 1 MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEEDQFSQNPISCFEWMFPGIIGAGL 60
 DB 1 MTCCEGWTSCNGFSLVLLVLLGVVLAIPILVSLVEEDQFSQNPISCFEWMFPGIIGAGL 60

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QY 61 MAIPATMTSLTARKRACCNRTGMPFLSPFSVITVIGALYCMILSTOALLKGLMGNSSPS 120
DB 61 MAIPATMTSLTARKRACCNRTGMPFLSPFSVITVIGALYCMILSTOALLKGLMGNSSPS 120
QY 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
DB 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
QY 181 ENKGRHLHPSVFLGLLVGLLEVLFGLSQIVIGFGLGCLGVSKRRSQIV 229
DB 178 EDBRRHIFHSVFMISLLVGLLEVLFGLSQIVIGFGLGCLGVSKRRSQIV 226

RESULT 6
Q9D3R0 PRELIMINARY; PRT; 226 AA.
ID Q9D3R0;
AC Q9D3R0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033405M13 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI2630.
GN Name=1810018L02R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
[1]
[2]
[3]
[4]
[5]
SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RA Nature 420:563-573(2002).
[1]
[2]
[3]
[4]
[5]
SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA MEDLINE=20499374; Pubmed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komano H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes.";
RA Genome Res. 10:1617-1630(2000).
[1]
[2]
[3]
[4]
[5]
SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA MEDLINE=20530913; Pubmed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komano H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multicapillary sequencer.";

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RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Furumishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kaeukawa T., Kato H.,
RA Kawai J., Kojima Y., Komano H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saio H., Saio R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK017154; BMB30618.1;
DR WGI; WGI:1913511; 1810018L02R1k.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6 membrane.
DR Pfam; PF05805; L6 membrane; 1.
SQ SEQUENCE 226 AA; 24714 MW; 8B6EB5C2D1EDDC0 CRC64;

Query Match 75.1%; Score 912.5; DB 2; Length 226;
Best Local Similarity 73.8%; Pred. No. 1,6e-72;
Matches 169; Conservative 27; Mismatches 30; Indels 3; Gaps 2;

QY 1 MTCCEGWTSCNGFSLVILLVGLVNAIPLIYSLVEEDQFSONPISCFEWWFGIIGAGL 60
DB 1 MTCCEGWTSCNGFSLVILLVGLVNAIPLIYSLVEADSTQNPISCFEWWFGIIGAGL 60
QY 61 MAIPATMTSLTARKRACCNRTGMPFLSPFSVITVIGALYCMILSTOALLKGLMGNSSPS 120
DB 61 MAIPATMTSLTARKRACCNRTGMPFLSPFSVITVIGALYCMILSTOALLKGLMGNSSPS 120
QY 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
DB 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
QY 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
DB 121 NSNANCEPFLKXISDHPESFNIQWPFNDSCAPPTGKPKTSDNTYASGWRASFFHPDSE 180
QY 181 ENKGRHLHPSVFLGLLVGLLEVLFGLSQIVIGFGLGCLGVSKRRSQIV 229
DB 178 EDBRRHIFHSVFMISLLVGLLEVLFGLSQIVIGFGLGCLGVSKRRSQIV 226

RESULT 7
Q7SYW6 PRELIMINARY; PRT; 197 AA.
ID Q7SYW6;
AC Q7SYW6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tmsf4-prov protein.
DE Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=8355;
[1]
[2]
[3]
[4]
[5]
SEQUENCE FROM N.A.
RA TISSUE=Whole;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datsenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Prange T.E.,
RA Brownstein M.J., Udell T.B., Toshtyuk S., Carninci P., Pringle C.,
RA Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Girmann J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX Klein S., Strausberg R.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC054239; AAH54239.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR008661; L6 membrane.
 DR Pfam; PF05805; L6 membrane; 1.
 SQ SEQUENCE 197 AA; 20576 MW; 987CD56419EB7E39 CRC64;
 Query Match 15.0%; Score 182; DB 2; Length 197;
 Best Local Similarity 25.8%; Pred. No. 4,6e-08;
 Matches 59; Conservative 30; Mismatches 88; Indels 52; Gaps 8;
 QY 3 CCEGWTSCNGESLIVLLGLVNAIPILVSLVEDEDSQNPISCFEMWFGIIGAGLMA 62
 DB 2 CCGGCACACGCTTLLPILALICLANILFFPGGTADK--NDHIDEVWYFGIVSGVLM 59
 QY 63 IPATMISLTARKRAC-----CNRTGMFLSFSFVITYGALYCMILISQALLKGPL 114
 DB 60 ITPALVFLGLKNNDCGCCGSCGKRPMTSITIPAIGVGAGYCTIVSAVAIDKGP 118
 QY 115 MCNSPNSNANCFESLNISDIPESFNLQWFNDSCAPPTGFNKPSTNDTMASGWRAS 174
 DB 119 -----KCDRGNGNYTVAQET-ELSW--KDCVEPPN-----ISEMWTL 154
 QY 175 FHPDSENRKRLHFSVFLGLLVGLVLEGLSQIVYIGFGLCCGVSK 223
 DB 155 F-----CLTLLMSGVQAVLCAL-QAINGLIGTICDCK 186
 RESULT 8
 Q6FHF6 PRELIMINARY; PRT; 197 AA.
 AC Q6FHF6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE TM4SF5 protein (Fragment).
 GN Name=TM4SF5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hallbeck A., Ebert L., Mkundinya M., Schick M., Risenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, CRS411798; CAG46597.1; -
 DR InterPro; IPR008661; L6 membrane.
 DR Pfam; PF05805; L6 membrane; 1.
 FT NON TER 197
 SQ SEQUENCE 197 AA; 20867 MW; 1EBB515EDD11075C CRC64;

Query Match 14.2%; Score 173; DB 2; Length 197;
 Best Local Similarity 27.7%; Pred. No. 2,9e-07;
 Matches 64; Conservative 32; Mismatches 87; Indels 48; Gaps 9;
 QY 3 CCEGWTSCNGESLIVLLGLVNAIPILVSLVEDEDSQNPISCFEMWFGIIGAGLMA 62
 DB 2 CTGACARVGSITLLGICIVANAL-LLVNGETSWNTNTHLSIQVLMGFCIGGLMV 60
 QY 63 IPATMISLTARKR-----ACNRTGMFLSFSFVITYGALYCMILISQALLKGPLMCN 117
 DB 61 LCPGIAAVRAGKCCGAGCCGNCRCMLRSVFSSAFGLAIVCLSVSGAGLRNGP---- 116
 QY 118 SPNSNANCFESLNISDIPESFNLQWFNDSCAPPTGFNKPSTNDTMASGWRASPFH 177
 DB 117 -----RC-----LMNGEWGTH-----FEDT-AGATVLLNRTLM 142
 QY 178 DSEENKRLHFSVFLGLLV--GILE-VLFGLSQIVYIGFGLCCGVSKRR 225
 DB 143 DRCEAPPRVPMVNTLFSLLVAASCLFIVLGI-QLVNATIGVFCGDKKK 192
 RESULT 9
 Q6IB79 PRELIMINARY; PRT; 197 AA.
 AC Q6IB79;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE TM4SF5 protein (Transmembrane 4 superfamily member 5).
 GN Name=TM4SF5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Girmann J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, CR456925; CAG33206.1; -
 DR EMBL, BC069519; AAH69519.1; -
 DR InterPro; IPR008661; L6 membrane.
 DR Pfam; PF05805; L6 membrane; 1.
 KW Transmembrane.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228814; PubMed=1565644;
RA Marken J.S., Schieven G.L., Hellstroem I., Hellstroem K.E., Arnolfo A.;
RT "Cloning and expression of the tumor-associated antigen L6.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3503-3507(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, and lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schermer A., Schein J.B., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP TOPOLOGY
RX MEDLINE=94117160; PubMed=7510285;
RA Marken J.S., Bajorath J., Edwards C.P., Farr A.G., Schieven G.L.,
RA Hellstrom I., Hellstrom K.E., Arnolfo A.;
RT "Membrane topology of the L6 antigen and identification of the protein
epitope recognized by the L6 monoclonal antibody.";
RL J. Biol. Chem. 269:7397-7401(1994).
CC -|- SUBUNIT: Present in high molecular weight complexes in tumor
cells.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Highly expressed on lung, breast, colon, and
ovarian carcinomas. It is also present on some normal cells,
endothelial cells in particular.
CC -|- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -|- This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See <http://www.ldb-sib.ch/announce/>
or send an email to license@ldb-sib.ch).

DR EMBL: M90657; AAA36158.1; -;
DR EMBL: BC008442; AA080442.1; -;
DR EMBL: BC010166; AA010166.1; -;
DR PIR: A42926; A42926.
DR Genew: HGNC:11853; TM4SF1.
DR MIM: 191155; -;
DR GO: GO:0005867; C: integral to plasma membrane; IDA.
DR InterPro: IPR008661; I6_membrane.
DR Pfam: PF05805; I6_membrane; 1.
KM Antigen; Glycoprotein; Transmembrane.
FT DOMAIN 1 9 Cytoplasmic (Probable).
FT TRANSMEM 10 30 Probable.
FT DOMAIN 31 49 Extracellular (Probable).
FT TRANSMEM 50 70 Probable.
FT DOMAIN 71 93 Cytoplasmic (Probable).
FT TRANSMEM 94 114 Probable.
FT DOMAIN 115 161 Extracellular (Probable).
FT TRANSMEM 162 182 Probable.

FT DOMAIN 183 202 Cytoplasmic (Probable).
FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 202 AA; 21632 MW; 80D82C47902B8CD4 CRC64;
Query Match 14.0%; Score 170; DB 1; Length 202;
Best Local Similarity 27.4%; Pred. No. 5.4e-07;
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;
QY 10 CNGFSLVLLLVGLVLAIPDIVSLVEEDQFQNPISCFEWMFGIIGAG-IMAIPTM 68
DB 9 CIGSLVGLALLCIAAN-ILLYFPNGETKVASENHLSRFVFGIVGGILMLPAFVF 67
QY 69 SLTRKAKAC-----CNRRTGMPLSSFFSYITVYIGALYCMILSIQALLKGPLMGNPSN 121
DB 68 IGLERDQCCCGCGHENGCKRCAMLSVLAALIGAGSYCYVALGIAEGPLCIDSLG- 126
QY 122 SNANCEFSLKNIISDIHPSEFNLQWFPNDSCAPPTGPNKPTSDNTMASGWRASFFHDS- 180
DB 127 -----QW-----NYTFAS--TEGQYLLDTST 145
QY 181 -----ENKHL-IPHSVFLGLLVGILEVLFGLSQIVIGFGLCG 220
DB 146 WSECTEPKHIVEMWVSLFSLALAGIEFIQLIQLVINGVLGIGCG 191
RESULT 13
CAG33234
ID CAG33234 PRELIMINARY; PRT; 202 AA.
AC CAG33234;
DT 01-JUN-2004 (TRENDSrel. 27, Created)
DT 01-JUN-2004 (TRENDSrel. 27, Last sequence update)
DT 01-JUN-2004 (TRENDSrel. 27, Last annotation update)
DS TM4SF1 protein.
GN TM4SF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway (TM) system entry
vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR456953; CAG33234.1; -;
SQ SEQUENCE 202 AA; 21632 MW; 80D82C47902B8CD4 CRC64;
Query Match 14.0%; Score 170; DB 2; Length 202;
Best Local Similarity 27.4%; Pred. No. 5.4e-07;
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;
QY 10 CNGFSLVLLLVGLVLAIPDIVSLVEEDQFQNPISCFEWMFGIIGAG-IMAIPTM 68
DB 9 CIGSLVGLALLCIAAN-ILLYFPNGETKVASENHLSRFVFGIVGGILMLPAFVF 67
QY 69 SLTRKAKAC-----CNRRTGMPLSSFFSYITVYIGALYCMILSIQALLKGPLMGNPSN 121
DB 68 IGLERDQCCCGCGHENGCKRCAMLSVLAALIGAGSYCYVALGIAEGPLCIDSLG- 126
QY 122 SNANCEFSLKNIISDIHPSEFNLQWFPNDSCAPPTGPNKPTSDNTMASGWRASFFHDS- 180
DB 127 -----QW-----NYTFAS--TEGQYLLDTST 145
RESULT 14
Q8NE91
ID Q8NE91 PRELIMINARY; PRT; 232 AA.
AC Q8NE91;

DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE TM4SF1 protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034145; AAI34145.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR InterPro; IPR008661; I6_membrane.
 DR Pfam; PF05805; I6_membrane; 1.
 SQ SEQUENCE 232 AA; 25057 MW; 90FA2DA611801B84 CRC64;
 QY Query Match 14.0%; Score 170; DB 2; Length 232;
 Best Local Similarity 27.4%; Pred. No. 6.3e-07;
 Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;
 QY 10 CNGFSLVLLILGVNLAIPIVLIVSEEDQFSQNPISCFEWWPFGIIGAG-LMAIPATM 68
 Db 9 CIGSLVGLALICIAAN-ILYFPNGETKVASSENHLRFVWFSGIVGGGLMLLPVVF 67
 QY 69 SLTRAKKAC-----CNRRTGMFLSFFSVITVIGALYCMILSIQALLKPLMKNSSPSN 121
 Db 68 IGLBDDDCGCGCGHNCCKRCAMLSSVLAALIGAGSYCVIVALGLAEPPLCIDISG- 126
 QY 122 SNANCEFSLKNIISDIHPSFNLOWFFNDSCAPPTGFNKTNSDNTWASGRASSPHFDS- 180
 Db 127 -----QW-----NYTFAS--TEGQYLLDTST 145
 QY 181 -----ENKRL-IHPSVFLGLVGLVLEFGLSQIVIGFGLCG 220
 Db 146 WSECTEPHIVEMNVSLFSILLALGIEFIILCIQVINGVIGIG 191
 RESULT 15
 Q6DHT3 PRELIMINARY; PRT; 201 AA.
 AC Q6DHT3;
 DT 01-OCT-2004 (Tremblrel. 28, Created)
 DT 01-OCT-2004 (Tremblrel. 28, Last sequence update)
 DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075884; AAI75884.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 201 AA; 21415 MW; 62E7CDD6D75A155 CRC64;
 QY Query Match 13.9%; Score 169; DB 2; Length 201;
 Best Local Similarity 26.4%; Pred. No. 6.6e-07;
 Matches 58; Conservative 31; Mismatches 89; Indels 42; Gaps 8;
 QY 12 GFSILVLLILGVNLAIPIVLIVSEEDQFSQNPISCFEWWPFGIIGAGLMAIPATM 71
 Db 11 GLMLPSAFLISTAN--LILFPNGEQDITKXISIQWLMGILGGLIMPCSCAIR 67
 QY 72 ARKR-----ACNRRRTGMFLSFFSVITVIGALYCMILSIQALLKPLMKNSSPSNANC 126
 Db 68 AGKKGCCGACCCGNRCMLNSVPSLSFGVIGSYCACVAIALAVGP-----KC 116
 QY 127 EFSIKNISDIHPSFNLOWFFNDSCAPPTGFNKTNSDNTWASGRASSPHFDS- 185
 Db 117 QV-----EGEIDWRY-----PFEDRKGNSSYLVDKSSWSECIY---PENM-V 154
 QY 186 LIHPSVFLGLVGLVLEFGLSQIVIGFGLCGVSKR 225
 Db 155 LMHIVLPSILLISALQAVLCVQVNGVCVGCICGDCRKR 194

Search completed: January 24, 2005, 16:00:00
 Job time : 258 secs

Tue Jan 25 10:13:11 2005

us-10-063-553-48.rpr

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:43:07 ; Search time 40 Seconds
(without alignments)
550.841 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSLVLL.....IVIGFLGCLGCVSRNQIV 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	14.0	202	2 A42926	L6 surface protein
2	166	13.7	197	2 UC6544	tumor-associated a
3	160	13.2	202	2 A53399	L6 antigen - mouse
4	136	11.2	202	2 UC6435	tumor-associated L
5	133	10.9	202	2 UC6205	cell surface antig
6	90.5	7.4	610	2 A85870	probable transport
7	90.5	7.4	610	2 H91025	probable transport
8	90.5	7.4	610	2 B65001	probable transport
9	89.5	7.4	319	2 A81298	formate dehydrogen
10	88.5	7.3	319	2 T33261	hypothetical prote
11	88	7.2	1036	2 A82357	probable multidrug
12	86.5	7.1	891	2 B82495	probable NADH dehy
13	86	7.1	283	2 A13340	maltoedextrin ABC-t
14	86	7.1	438	2 H64713	Na+/H+-exchanging
15	85.5	7.0	271	2 B82295	prolipoprotein dia
16	85.5	7.0	457	2 T46332	hypothetical prote
17	85	7.0	283	2 A11710	maltoedextrin ABC-t
18	85	7.0	379	2 S58057	hypothetical prote
19	84.5	7.0	281	2 T51961	XRRI-like protein
20	84	6.9	286	2 AC0848	iron transport pro
21	84	6.9	438	2 B71805	Na+/H+-exchanging
22	83	6.8	332	2 T33258	hypothetical prote
23	82	6.7	858	2 T08881	prominin - mouse
24	81.5	6.7	494	2 T32644	hypothetical prote
25	81	6.7	254	2 S20741	chitinase (EC 3.2.
26	81	6.7	461	2 T55671	hypothetical prote
27	80	6.6	379	1 S17418	ubiquinol-cytochro
28	80	6.6	721	2 AH3417	lipa protein (limp
29	79.5	6.5	369	2 T24620	hypothetical prote

30	79.5	6.5	558	2 T47505	hypothetical prote
31	79.5	6.5	608	2 AC0798	probable sodium/su
32	79.5	6.5	1143	2 T10636	hypothetical prote
33	79	6.5	1353	2 JC4279	adenylate cyclase
34	78.5	6.5	363	2 AH2796	hypothetical prote
35	78.5	6.5	363	2 H97575	probable permease
36	78	6.4	309	2 C89831	conserved hypotnet
37	78	6.4	1062	2 F83335	RND multidrug effl
38	78	6.4	1062	2 T30830	hypothetical prote
39	78	6.4	1783	2 T37258	probable voltage-d
40	78	6.4	1917	2 C88728	protein C48A7.1 (i
41	77.5	6.4	459	2 T11489	NADH2 dehydrogenas
42	77.5	6.4	459	2 A89785	hexose phosphate t
43	77.5	6.4	500	2 C70175	L-lactate permease
44	77.5	6.4	557	2 JC5487	cellulase (EC 3.2.
45	77	6.3	347	2 T15672	hypothetical prote
46	77	6.3	1032	2 H64100	acetylavine resist
47	77	6.3	1215	2 C84848	hypothetical prote
48	76.5	6.3	379	2 T11505	ubiquinol-cytochro
49	76.5	6.3	451	2 B70792	hypothetical prote
50	76.5	6.3	538	2 T47624	hypothetical prote
51	76.5	6.3	614	2 S78277	diak-type molecula
52	76	6.3	346	2 T28718	hypothetical prote
53	76	6.3	431	2 AD1237	arsenic efflux pun
54	76	6.3	447	2 D90012	hypothetical prote
55	76	6.3	531	2 B69821	multidrug resistan
56	76	6.3	561	2 T23564	hypothetical prote
57	76	6.3	604	2 T31042	hypothetical prote
58	76	6.3	824	2 T15230	hypothetical prote
59	76	6.3	1011	2 T13669	neuromusculin - fr
60	75.5	6.2	384	2 T11931	ubiquinol-cytochro
61	75.5	6.2	409	2 AG0362	manganese transpor
62	75.5	6.2	476	2 A84454	hypothetical prote
63	75.5	6.2	788	2 S48191	probable ubiquinol
64	75.5	6.2	824	1 S50767	S-receptor kinase
65	75.5	6.2	1106	2 T11948	hypothetical prote
66	75	6.2	373	2 A11832	hypothetical prote
67	75	6.2	379	2 I49399	ubiquinol-cytochro
68	75	6.2	385	2 G82789	permease XFO589 (i
69	75	6.2	581	2 I45971	prolactin receptor
70	75	6.2	1015	2 T15830	hypothetical prote
71	75	6.2	2201	2 A32160	tenascin-C - human
72	74.5	6.1	254	2 S19390	arsenic pump mem
73	74.5	6.1	429	1 B41902	hypothetical prote
74	74.5	6.1	432	2 A97832	tetracycline resist
75	74.5	6.1	458	2 S23743	arginine/ornithine
76	74.5	6.1	468	2 H82321	hypothetical prote
77	74.5	6.1	618	2 F86149	ubiquinol-cytochro
78	74	6.1	379	1 S17406	ubiquinol-cytochro
79	74	6.1	379	2 I49400	arsenic efflux pun
80	74	6.1	431	2 A11599	probable transport
81	74	6.1	555	2 T47512	prominin - rat
82	74	6.1	857	2 JC7716	ubiquinol - cytochro
83	73.5	6.0	380	2 S70594	hypothetical prote
84	73.5	6.0	387	2 B84721	arsenic pump mem
85	73.5	6.0	429	1 C41903	uncharacterized me
86	73.5	6.0	544	2 C96943	maltoese/maltoedextr
87	73	6.0	280	2 D84015	hypothetical prote
88	73	6.0	298	2 R87570	ubiquinol-cytochro
89	73	6.0	413	2 S17413	aspartate transami
90	73	6.0	413	2 S01076	tetracycline resist
91	73	6.0	458	1 YTB5RT	tetracycline resist
92	73	6.0	458	1 YTB5RT	tetracycline resist
93	73	6.0	458	1 YTB5RT	tetracycline resist
94	73	6.0	458	2 QJ1211	tetracycline resist
95	73	6.0	501	2 H89844	hypothetical prote
96	73	6.0	582	2 T05020	L-ascorbate oxidas
97	73	6.0	718	2 A42163	Na+/myo-inositol c
98	73	6.0	1291	1 A28334	protein-tyrosine-p
99	72.5	6.0	215	2 JU0385	hypothetical 22.6k
100	72.5	6.0	215	2 AH1863	hypothetical prote
101	72.5	6.0	275	2 C89858	conserved hypotnet
102	72.5	6.0	290	2 T06856	hypothetical prote

103	72.5	6.0	397	2	S49301	176	70	5.8	520	2	E86200	protein f12k1.18
104	72.5	6.0	575	2	A54861	177	70	5.8	544	2	T27444	hypothetical prote
105	72.5	6.0	598	2	T32166	178	70	5.8	557	2	T47506	hypothetical prote
106	72.5	6.0	606	2	T27072	179	70	5.8	710	2	B71417	hypothetical prote
107	72.5	6.0	616	2	S50998	180	70	5.8	795	2	T21487	hypothetical prote
108	72.5	6.0	904	2	T40072	181	70	5.8	1083	2	S54293	regulator protein
109	72.5	6.0	1267	2	T21340	182	70	5.8	1748	1	QJ1555	gene polyprotein
110	72.5	5.9	344	2	S42648	183	70	5.8	2049	1	T43161	sodium channel pro
111	72	5.9	344	2	AB2306	184	70	5.7	158	2	H71902	phosphatidylglyce
112	72	5.9	378	2	S19007	185	69.5	5.7	221	2	AE2537	two-component resp
113	72	5.9	441	2	D85647	186	69.5	5.7	283	2	B86902	channel protein vi
114	72	5.9	441	2	D90787	187	69.5	5.7	347	2	AD3513	hypothetical prote
115	72	5.9	441	2	D64844	188	69.5	5.7	356	2	T22882	hypothetical prote
116	72	5.9	447	2	B95369	189	69.5	5.7	474	2	AI1821	protein-export mem
117	72	5.9	475	2	T19486	190	69.5	5.7	551	2	AB7019	probable cytochrom
118	72	5.9	607	2	T26845	192	69.5	5.7	669	2	B34285	NADH2 dehydrogenas
119	72	5.9	617	2	T01227	193	69.5	5.7	675	2	D85065	receptor protein k
120	72	5.9	982	2	B88465	194	69.5	5.7	702	2	E64250	cell division prot
121	72	5.9	1253	2	T21065	195	69.5	5.7	724	2	A42953	nitrous oxide redu
122	72	5.9	1583	2	S59644	196	69.5	5.7	832	2	S56823	probable membrane
123	71.5	5.9	363	2	H71335	197	69.5	5.7	1018	2	E83099	probable RND efflu
124	71.5	5.9	366	2	C64449	198	69.5	5.7	1817	2	T34249	hypothetical prote
125	71.5	5.9	386	2	AD0218	199	69.5	5.7	2019	1	QJ1322	tenascin precursor
126	71.5	5.9	398	2	JN0708	200	69	5.7	202	2	T26214	hypothetical prote
127	71.5	5.9	444	2	G70042	201	69	5.7	216	2	A54305	KRAG protein - mou
128	71.5	5.9	495	2	T12401	202	69	5.7	231	2	C64826	aquaporin Z - Bach
129	71.5	5.9	581	2	S03540	203	69	5.7	231	2	A99749	transmembrane wate
130	71.5	5.9	784	2	AB6676	204	69	5.7	231	2	E85599	prolipo-protein dia
131	71.5	5.9	880	2	AT1179	205	69	5.7	283	2	CH1124	probable membrane
132	71.5	5.9	1029	2	C97665	206	69	5.7	285	2	AI0633	hypothetical prote
133	71.5	5.9	1029	2	C97665	207	69	5.7	300	2	B69072	hypothetical prote
134	71.5	5.9	1043	2	AB0370	208	69	5.7	303	2	T31909	hypothetical prote
135	71	5.8	344	2	B95050	209	69	5.7	309	2	T34080	hypothetical prote
136	71	5.8	345	2	B95050	210	69	5.7	355	2	D71429	hypothetical prote
137	71	5.8	430	2	G89562	211	69	5.7	371	2	B86489	protein T32E20.25
138	71	5.8	487	2	B27255	212	69	5.7	377	2	T11361	ubiquinol-cytochro
139	71	5.8	614	2	T29337	213	69	5.7	397	2	F83385	probable MFS trans
140	71	5.8	708	2	T19569	214	69	5.7	426	2	T20253	hypothetical prote
141	71	5.8	712	2	AG1888	215	69	5.7	475	2	T46745	arginine/ornithine
142	71	5.8	1246	2	C63680	216	69	5.7	494	2	A82294	probable carbon sc
143	70.5	5.8	129	2	S40363	217	69	5.7	513	2	B81217	virulence factor M
144	70.5	5.8	141	2	T11270	218	69	5.7	519	2	E70784	cytochrome b homol
145	70.5	5.8	229	1	ICBO	219	69	5.7	617	2	T02668	probable receptor
146	70.5	5.8	230	1	A95034	220	69	5.7	622	2	AI1453	bacteriophage mino
147	70.5	5.8	236	2	A97905	221	69	5.7	678	2	B71308	hypothetical prote
148	70.5	5.8	239	2	T48120	222	69	5.7	692	2	H71494	probable thiol-dis
149	70.5	5.8	282	1	SAVL64	223	69	5.7	709	2	S75212	com. protein - syn
150	70.5	5.8	352	2	150047	224	69	5.7	814	2	T05537	probable serine/ch
151	70.5	5.8	374	2	C83078	225	69	5.7	829	2	AB1536	cation (calcium) t
152	70.5	5.8	379	2	A53077	226	69	5.7	882	2	AB1536	probable membrane
153	70.5	5.8	420	2	T47998	227	69	5.7	971	2	A37860	calcium channel pr
154	70.5	5.8	446	2	T35005	228	69	5.7	1852	2	A37860	cell surface glyco
155	70.5	5.8	477	2	A87285	229	69.5	5.6	176	2	I53630	MHC class II histo
156	70.5	5.8	506	2	F83369	230	69.5	5.6	269	2	D90670	hypothetical prote
157	70.5	5.8	522	2	B81584	231	69.5	5.6	306	2	G85520	hypothetical prote
158	70.5	5.8	591	2	C86538	232	69.5	5.6	361	2	T45918	hypothetical prote
159	70.5	5.8	591	2	C86538	233	69.5	5.6	369	2	I64234	competence locus E
160	70.5	5.8	594	2	B72086	234	69.5	5.6	374	2	T09771	phosphatidate cycl
161	70.5	5.8	760	2	S19374	235	69.5	5.6	379	1	S43262	ubiquinol-cytochro
162	70.5	5.8	1056	2	A53767	236	69.5	5.6	426	1	SAVL6	large surface anti
163	70.5	5.8	1583	2	F86366	237	69.5	5.6	443	2	C70818	probable ABC trans
164	70.5	5.8	2051	2	T13364	238	69.5	5.6	452	1	D69810	phosphotransferase
165	70	5.8	185	2	A70075	239	69.5	5.6	454	2	AC1413	PTS system, cellob
166	70	5.8	253	2	B89779	240	69.5	5.6	454	2	AB1789	PTS system, cellob
167	70	5.8	255	2	B81197	241	69.5	5.6	469	2	C90446	permease, multidu
168	70	5.8	283	2	E81895	242	69.5	5.6	511	2	G64902	extreme acid resis
169	70	5.8	379	1	S17419	243	69.5	5.6	511	2	A90891	acid sensitivity p
170	70	5.8	379	2	T48180	244	69.5	5.6	511	2	H85726	acid sensitivity p
171	70	5.8	379	2	S58460	245	69.5	5.6	627	2	T11125	NADH2 dehydrogenas
172	70	5.8	437	2	E84619	246	69.5	5.6	643	2	C90025	hypothetical prote
173	70	5.8	490	2	S52830	247	69.5	5.6	643	2	QJ2150	hypothetical prote
174	70	5.8	510	2	C64883	248	69.5	5.6	643	2	QJ2150	hypothetical prote
175	70	5.8	512	2	E81794							

249	68.5	5.6	1016	2	F82159	transporter, Acrb/
250	68.5	5.6	1091	2	G59435	DIC-1 (deleted in
251	68.5	5.6	1500	2	T03824	probable immediate
252	68	5.6	206	2	S08632	nodulin-21 - soybe
253	68	5.6	228	2	G82400	tons system transp
254	68	5.6	312	2	G69423	branched-chain ami
255	68	5.6	379	1	S17405	ubiquitinol-cytochro
256	68	5.6	379	1	S17409	ubiquitinol-cytochro
257	68	5.6	379	2	I48133	ubiquitinol-cytochro
258	68	5.6	379	2	S58451	ubiquitinol-cytochro
259	68	5.6	379	2	S58447	ubiquitinol-cytochro
260	68	5.6	405	2	T44249	transport protein
261	68	5.6	423	2	S74046	probable sugar tra
262	68	5.6	425	2	G91082	probable transport
263	68	5.6	425	2	H85927	probable transport
264	68	5.6	425	2	G65059	probable transport
265	68	5.6	443	2	G65008	hypothetical prote
266	68	5.6	443	2	B82171	probable sodium-de
267	68	5.6	465	2	B17176	transhydrogenase c
268	68	5.6	498	2	A48203	interleukin-14 pre
269	68	5.6	504	2	S00390	ig gamma chain (cl
270	68	5.6	510	2	B97307	probable cardioliip
271	68	5.6	516	2	F82070	2-isopropylmalate
272	68	5.6	527	2	H85135	hypothetical prote
273	68	5.6	527	2	H83165	probable sodium/su
274	68	5.6	641	2	S44253	raffinose carrier
275	68	5.6	689	2	D85013	hypothetical prote
276	68	5.6	725	2	B82425	conserved hypothec
277	68	5.6	799	2	A48716	glycine transporte
278	68	5.6	865	2	B96558	probable protein x
279	68	5.6	926	2	T16184	hypothetical prote
280	68	5.6	1008	1	GNVUUK	glycoprotein precu
281	68	5.6	1247	1	G89583	protein K0783.1 [i
282	68	5.6	1810	1	A32230	tenascin precursor
283	68	5.6	3176	2	CGH03A	collagen alpha 3(V
284	67.5	5.6	120	2	A11727	hypothetical prote
285	67.5	5.6	197	2	B69447	hypothetical prote
286	67.5	5.6	208	2	B97899	hypothetical prote
287	67.5	5.6	228	2	T16678	hypothetical prote
288	67.5	5.6	229	1	LCSH	prolactin precursor
289	67.5	5.6	261	2	I68718	MHC class II histo
290	67.5	5.6	328	1	S25933	NMDH2 dehydrogenas
291	67.5	5.6	337	2	B88957	protein ZK697.7 [i
292	67.5	5.6	379	2	S58458	ubiquitinol-cytochro
293	67.5	5.6	386	2	G84386	oligopeptide trans
294	67.5	5.6	415	2	B84858	hypothetical prote
295	67.5	5.6	431	1	SAVL59	large surface anti
296	67.5	5.6	431	2	F90316	deep protein, prob
297	67.5	5.6	452	2	G95306	putrescine/ornithi
298	67.5	5.6	456	2	H86902	membrane protein,
299	67.5	5.6	472	2	T29313	regulates beta-lac
300	67.5	5.6	491	2	G90689	regulates beta-lac
301	67.5	5.6	491	2	C85540	signal transducer
302	67.5	5.6	491	2	S37391	probable membrane
303	67.5	5.6	509	2	S45413	probable sucrose c
304	67.5	5.6	548	2	T25401	hypothetical prote
305	67.5	5.6	553	2	T38541	hypothetical prote
306	67.5	5.6	556	2	T31884	G protein-coupled
307	67.5	5.6	907	2	T21612	hypothetical prote
308	67.5	5.6	955	2	F70746	probable mmp12 pro
309	67.5	5.6	968	2	A66449	multidrug efflux p
310	67.5	5.6	1041	2	AC0423	voltage-dependent
311	67.5	5.6	1610	2	A66227	calcium channel al
312	67.5	5.6	2161	2	JH0564	calcium channel al
313	67.5	5.6	2181	2	A38198	hypothetical prote
314	67.5	5.6	252	2	A86449	conserved hypothet
315	67	5.5	296	2	AH1173	hypothetical prote
316	67	5.5	314	2	T15519	hypothetical prote
317	67	5.5	360	2	T06786	6a-hydroxymaackiai
318	67	5.5	379	1	S17420	ubiquitinol-cytochro
319	67	5.5	379	1	S58085	ubiquitinol-cytochro
320	67	5.5	393	2	A39251	thyrotropin-releas
321	67	5.5	407	2	S37550	triase phosphate/3
322	67	5.5	408	2	S37553	triase phosphate/3
323	67	5.5	411	2	I56444	thyrotrophin-relea
324	67	5.5	411	2	T17653	hypothetical prote
325	67	5.5	412	2	S23436	thyrotliberin recep
326	67	5.5	428	2	S61186	glutamates 5-kinase
327	67	5.5	448	2	C96542	hypothetical prote
328	67	5.5	454	2	B85826	probable amino aci
329	67	5.5	454	2	H90980	probable amino aci
330	67	5.5	454	2	E64966	probable amino aci
331	67	5.5	462	2	S42372	hypothetical prote
332	67	5.5	466	2	T42254	amino acid permeas
333	67	5.5	518	2	S61920	B-alpha pheromone-
334	67	5.5	526	2	T23779	hypothetical prote
335	67	5.5	536	2	A71491	probable integral
336	67	5.5	537	2	H88087	protein B0454.4 [i
337	67	5.5	554	2	G96598	protein P20N2.6 [i
338	67	5.5	602	2	G97784	hypothetical prote
339	67	5.5	630	2	S46740	hypothetical prote
340	67	5.5	637	2	S01509	NMDH2 dehydrogenas
341	67	5.5	685	2	S67146	probable membrane
342	67	5.5	792	2	G84830	probable potassium
343	67	5.5	992	2	S49835	hypothetical prote
344	67	5.5	2958	2	S64921	probable membrane
345	66.5	5.5	229	1	LCFG	prolactin precursor
346	66.5	5.5	234	2	T11914	cox1 intron protei
347	66.5	5.5	268	2	C71872	hypothetical prote
348	66.5	5.5	319	2	AF0489	probable iron tran
349	66.5	5.5	407	2	A69188	ammonium transport
350	66.5	5.5	410	2	C64618	conserved hypothec
351	66.5	5.5	482	2	T02538	hypothetical prote
352	66.5	5.5	489	2	B69833	metabolite permeas
353	66.5	5.5	489	2	T24971	hypothetical prote
354	66.5	5.5	705	2	S23352	gene unc-93 protei
355	66.5	5.5	719	2	T00286	hypothetical prote
356	66.5	5.5	937	2	A56517	nucleoporin Nup98
357	66.5	5.5	1078	2	A56715	calcium receptor (
358	66.5	5.5	1088	2	B56715	calcium receptor (
359	66.5	5.5	3391	1	GNMV16	genome polyprotein
360	66.5	5.5	4981	1	T18489	hypothetical prote
361	66	5.4	218	1	A43522	23k integral membr
362	66	5.4	222	2	F64563	hypothetical prote
363	66	5.4	238	2	A45544	Bola-QQ beta-1 - b
364	66	5.4	239	2	S64327	probable membrane
365	66	5.4	255	2	F81833	conserved hypothet
366	66	5.4	271	2	AC1692	hypothetical prote
367	66	5.4	295	2	C70166	hypothetical prote
368	66	5.4	339	2	T22195	hypothetical prote
369	66	5.4	342	2	A40191	platelet-activatin
370	66	5.4	348	2	E82896	hemim permease Uu3
371	66	5.4	352	2	JR0296	thyrotropin releas
372	66	5.4	373	2	S54545	hypothetical prote
373	66	5.4	379	1	CBBO	ubiquitinol-cytochro
374	66	5.4	379	2	T11259	ubiquitinol-cytochro
375	66	5.4	381	1	CBMS	ubiquitinol-cytochro
376	66	5.4	383	2	S54213	flagellar biosynuch
377	66	5.4	402	2	T29703	hypothetical prote
378	66	5.4	413	2	H82270	hypothetical prote
379	66	5.4	414	2	S34829	triase phosphate/3
380	66	5.4	414	2	S23224	triase phosphate/3
381	66	5.4	422	2	D72302	hypothetical prote
382	66	5.4	422	2	B82904	hypothetical prote
383	66	5.4	444	2	S62414	probable ubiquitin
384	66	5.4	447	2	AI0701	probable amino aci
385	66	5.4	482	2	A39285	calcitonin recepto
386	66	5.4	498	2	I47130	calcitonin recepto
387	66	5.4	505	2	F90427	amino acid transpo
388	66	5.4	581	2	S17150	potassium channel
389	66	5.4	583	2	A25096	NMDH2 dehydrogenas
390	66	5.4	598	2	B70036	capsular polysacch
391	66	5.4	609	2	T11310	NMDH2 dehydrogenas
392	66	5.4	611	2	S09142	NOS intoron 1 prote
393	66	5.4	650	2	S23217	beta-fructofuranos
394	66	5.4	674	2	T21217	hypothetical prote

395	66	5.4	689	2	T11917	MADH2 dehydrogenas	468	65	5.3	487	2	C82215	probable transport
396	66	5.4	718	2	A56851	Na+/K+-ATPase	469	65	5.3	509	2	A33801	muscle-fat glucose
397	66	5.4	754	2	A11627	protein-export mem	470	65	5.3	563	2	T44214	probable phosphotr
398	66	5.4	770	2	S60676	cellobiose oxidase	471	65	5.3	563	2	T44029	ganciclovir kinase
399	66	5.4	877	2	C46356	env polyprotein -	472	65	5.3	580	2	A56382	purine permease, b
400	66	5.4	893	2	S64926	probable membrane	473	65	5.3	616	2	T03027	receptor-like prot
401	66	5.4	1034	2	D65119	acetylflavin resista	474	65	5.3	652	2	H96924	probable phosphoty
402	66	5.4	1217	2	T00270	hypothetical prote	475	65	5.3	667	2	S51763	sulfate transport
403	66	5.4	1218	2	T30293	ABC transport prot	476	65	5.3	728	2	C75601	cation-transportin
404	66	5.4	1615	2	JB0372	low density lipopr	477	65	5.3	754	2	AG1265	protein-export mem
405	65.5	5.4	83	2	AG3378	hypothetical membr	478	65	5.3	826	2	E81706	conserved hypotet
406	65.5	5.4	139	2	G32536	T-cell receptor al	479	65	5.3	1018	1	GNMXG7	genome polyprotein
407	65.5	5.4	226	1	UX0221	C9g antigen - Dovi	480	65	5.3	1042	2	I50099	H,K-ATPase - giant
408	65.5	5.4	229	2	AG1133	prolactin precursor	481	65	5.3	1106	2	T25065	hypothetical prote
409	65.5	5.4	233	2	H82944	thymidylate kinase	482	65	5.3	1219	2	T06608	disease resistance
410	65.5	5.4	258	2	A29088	Smh class II histo	483	65	5.3	1231	2	E90182	hypothetical prote
411	65.5	5.4	259	2	S64423	probable membrane	484	65	5.3	2195	2	T34264	hypothetical prote
412	65.5	5.4	261	1	HLH0D8	MHC class II histo	485	64.5	5.3	125	2	JH0184	hydrophobin Sc3 pr
413	65.5	5.4	277	2	D42400	membrane protein M	486	64.5	5.3	154	2	T18204	hypothetical prote
414	65.5	5.4	279	2	AB1745	conserved hypotet	487	64.5	5.3	163	2	B84731	hypothetical prote
415	65.5	5.4	279	2	AD1375	conserved hypotet	488	64.5	5.3	191	2	AD2040	hypothetical prote
416	65.5	5.4	293	1	QOCVHV	BI1 protein - aqua	489	64.5	5.3	197	2	B81720	conserved hypotet
417	65.5	5.4	342	2	AD2367	hypothetical prote	490	64.5	5.3	218	2	G71260	probable ribulose-
418	65.5	5.4	361	2	T13259	hypothetical prote	491	64.5	5.3	218	2	F81111	nickel-dependent h
419	65.5	5.4	379	1	S43261	ubiquinol-cytochro	492	64.5	5.3	220	2	D71946	hypothetical prote
420	65.5	5.4	379	1	S43265	ubiquinol-cytochro	493	64.5	5.3	229	2	I83982	prolactin - goat
421	65.5	5.4	379	1	S43265	ubiquinol-cytochro	494	64.5	5.3	229	2	I45942	MHC class II - bov
422	65.5	5.4	379	1	S58459	ubiquinol-cytochro	495	64.5	5.3	253	2	B34801	pathogenesis-relat
423	65.5	5.4	380	1	S73751	high affinity tran	496	64.5	5.3	261	2	I45928	MHC class II - bov
424	65.5	5.4	405	2	C71462	hypothetical prote	497	64.5	5.3	305	2	S29711	olfactory factor O
425	65.5	5.4	435	2	AC0104	probable sugar tra	498	64.5	5.3	321	2	A10007	lipopolysaccharide
426	65.5	5.4	529	2	T22398	hypothetical prote	499	64.5	5.3	322	2	C83562	hypothetical prote
427	65.5	5.4	530	1	A56841	glucose-6-phosphat	500	64.5	5.3	326	2	G84748	hypothetical prote
428	65.5	5.4	534	2	A37483	F protein - Muraya	501	64.5	5.3	330	2	T43061	hypothetical prote
429	65.5	5.4	587	2	D84426	hypothetical prote	502	64.5	5.3	331	1	DNOB01	MADH2 dehydrogenas
430	65.5	5.4	620	2	T49067	transcription fact	503	64.5	5.3	331	2	F89771	lipoprotein [lipor
431	65.5	5.4	656	2	B49423	semaphorin I - fru	504	64.5	5.3	340	2	E83126	ferric enterobacti
432	65.5	5.4	806	2	C86445	hypothetical prote	505	64.5	5.3	346	2	AH3563	ribose transport s
433	65.5	5.4	856	1	A44963	env polypeptide pr	506	64.5	5.3	372	2	AG1834	NADH dehydrogenase
434	65.5	5.4	868	2	T13257	hypothetical prote	507	64.5	5.3	379	1	S43266	ubiquinol-cytochro
435	65.5	5.4	897	2	S67283	hypothetical prote	508	64.5	5.3	379	1	S43268	ubiquinol-cytochro
436	65.5	5.4	910	2	C69069	cation-transportin	509	64.5	5.3	379	2	S58466	ubiquinol-cytochro
437	65.5	5.4	928	2	S50578	hypothetical prote	510	64.5	5.3	385	2	I84455	dopamine transport
438	65.5	5.4	1029	2	D83120	probable RND efflu	511	64.5	5.3	393	2	A64036	hypothetical prote
439	65.5	5.4	1085	2	S40476	Ca(2+)-sensing rec	512	64.5	5.3	402	2	A64036	probable disease r
440	65.5	5.4	1246	2	T00826	hypothetical prote	513	64.5	5.3	431	1	SAVL71	large surface anti
441	65.5	5.4	1623	2	T01369	ABC transporter At	514	64.5	5.3	431	1	SAVL71	large surface anti
442	65.5	5.4	1737	2	T17101	probable voltage-a	515	64.5	5.3	435	2	C96779	arsenical pump mem
443	65.5	5.4	1816	2	A84845	probable ABC trans	516	64.5	5.3	441	2	C96779	protein serine car
444	65.5	5.4	2163	2	T15276	hypothetical prote	517	64.5	5.3	443	2	T20292	hypothetical prote
445	65	5.3	136	2	S05628	MADH2 dehydrogenas	518	64.5	5.3	454	2	AG0763	probable amino aci
446	65	5.3	172	2	E82464	probable acetyltra	519	64.5	5.3	464	2	T50785	nucleoid DNA-bindi
447	65	5.3	203	2	F91006	hypothetical prote	520	64.5	5.3	503	2	T38303	SWI/SNF complex tr
448	65	5.3	212	2	A12032	hypothetical prote	521	64.5	5.3	512	2	G90399	amino acid transpo
449	65	5.3	271	2	AH0161	probable membrane	522	64.5	5.3	561	2	A11408	potassium-transport
450	65	5.3	301	2	C69143	hypothetical prote	523	64.5	5.3	574	2	T41069	hypothetical prote
451	65	5.3	336	2	E64717	methicillin resist	524	64.5	5.3	620	2	I57937	dopamine transport
452	65	5.3	338	2	S50339	MADH2 dehydrogenas	525	64.5	5.3	620	2	A48980	dopamine transport
453	65	5.3	365	2	AE2782	transcription regu	526	64.5	5.3	634	2	T22351	hypothetical prote
454	65	5.3	365	2	F97561	hypothetical prote	527	64.5	5.3	639	2	H96693	hypothetical prote
455	65	5.3	373	2	G85355	nodulin-like prote	528	64.5	5.3	683	2	T03146	probable glycoprot
456	65	5.3	379	1	S41832	ubiquinol-cytochro	529	64.5	5.3	689	1	E70408	ferrous iron trans
457	65	5.3	379	1	S43263	ubiquinol-cytochro	530	64.5	5.3	724	2	D84377	protein export [im
458	65	5.3	379	2	T48134	ubiquinol-cytochro	531	64.5	5.3	803	2	S45916	hypothetical prote
459	65	5.3	379	2	S58452	ubiquinol-cytochro	532	64.5	5.3	879	2	D96802	MDR-type permease
460	65	5.3	379	2	E58851	ubiquinol-cytochro	533	64.5	5.3	858	2	A70634	probable mmp11 pro
461	65	5.3	379	2	S58448	ubiquinol-cytochro	534	64.5	5.3	1028	2	AD0052	probable multi-dru
462	65	5.3	389	2	B96522	hypothetical prote	535	64.5	5.3	1135	1	JQ1928	G2-g. polypeptide
463	65	5.3	400	2	E82367	probable multiting	536	64.5	5.3	1150	2	AB0064	probable membrane
464	65	5.3	410	2	C84176	oxalate/formate an	537	64.5	5.3	1165	1	S45879	chitin synthase [E
465	65	5.3	423	2	AG2394	hypothetical prote	538	64.5	5.3	1447	1	VG1HE3	E2 g.-ycoprotein pr
466	65	5.3	455	2	T16070	hypothetical prote	539	64.5	5.3	1447	1	VG1HE2	E2 g.-ycoprotein pr
467	65	5.3	473	2	S51256	probable membrane	540	64.5	5.3	1487	2	S62048	probable membrane

541	64.5	5.3	1495	2	E86428	probable ABC trans	614	63.5	5.2	308	2	T24453	hypothetical prote
542	64.5	5.3	1646	2	JH0422	voltage-dependent	615	63.5	5.2	350	2	C88987	protein C50H11.2 [
543	64.5	5.3	1687	2	T30244	phosphodiesterase	616	63.5	5.2	351	2	T23990	hypothetical prote
544	64.5	5.3	1719	2	T30174	exoribonuclease, v	617	63.5	5.2	367	2	C82943	ferrichrome ABC tr
545	64.5	5.3	1748	1	JN0786	integrin beta-4 ch	618	63.5	5.2	379	1	S17415	ubiquinol-cytochro
546	64.5	5.3	2203	2	T42742	voltage-dependent	619	63.5	5.2	379	2	T11492	ubiquinol-cytochro
547	64.5	5.3	2262	2	T30850	calcium channel al	620	63.5	5.2	379	2	T10998	ubiquinol-cytochro
548	64.5	5.3	159	2	G75555	conserved hypotet	621	63.5	5.2	385	2	H71960	hypothetical prote
549	64	5.3	167	2	I58352	p16INK4a - mouse	622	63.5	5.2	387	2	F82692	conserved hypotet
550	64	5.3	227	2	F96777	germin-like protei	623	63.5	5.2	389	2	H86266	hypothetical prote
551	64	5.3	232	2	S32398	serine proteinase	624	63.5	5.2	442	2	H81402	probable integral
552	64	5.3	253	2	AE2797	cytochrome c-type	625	63.5	5.2	446	2	H90094	hypothetical prote
553	64	5.3	254	2	AE4728	probable membrane	626	63.5	5.2	454	2	H91127	L-serine deaminase
554	64	5.3	261	2	T11486	cytochrome-c oxida	627	63.5	5.2	456	2	G85972	probable L-serine
555	64	5.3	267	2	E97576	cytochrome-c-type	628	63.5	5.2	458	1	VTB598	tetracycline resis
556	64	5.3	318	2	AH0499	probable phosphate	629	63.5	5.2	463	2	D69792	amino acid permeas
557	64	5.3	333	2	T02614	hypothetical prote	630	63.5	5.2	508	2	T21866	hypothetical prote
558	64	5.3	335	2	B71801	probable undecapre	631	63.5	5.2	521	2	C86678	hypothetical prote
559	64	5.3	350	2	E81303	probable branched-	632	63.5	5.2	522	2	T29705	hypothetical prote
560	64	5.3	355	1	A46191	iodopsin homolog -	633	63.5	5.2	531	2	T19232	hypothetical prote
561	64	5.3	357	2	C69233	anion permease - M	634	63.5	5.2	532	2	T52442	hypothetical prote
562	64	5.3	378	2	D64181	probable cytochrom	635	63.5	5.2	561	2	AH1785	potassium-transport
563	64	5.3	379	1	S17407	ubiquinol-cytochro	636	63.5	5.2	568	2	T31692	hypothetical prote
564	64	5.3	379	2	S58461	ubiquinol-cytochro	637	63.5	5.2	596	2	T17333	hypothetical prote
565	64	5.3	379	2	T11349	ubiquinol-cytochro	638	63.5	5.2	608	2	AG0846	formate hydrogently
566	64	5.3	382	2	A72373	conserved hypotet	639	63.5	5.2	610	2	F82192	ABC transporter. A
567	64	5.3	396	2	F96545	hypothetical prote	640	63.5	5.2	621	2	AF3016	Na+/H+ antiporter
568	64	5.3	405	2	A57479	amino acid transpo	641	63.5	5.2	642	2	B98268	probable sodium/hy
569	64	5.3	426	2	E71675	hypothetical prote	642	63.5	5.2	642	2	B98268	probable sodium/hy
570	64	5.3	426	2	T33775	hypothetical prote	643	63.5	5.2	698	2	T48432	meturase-like prot
571	64	5.3	444	2	JC1141	metacyclic-form-sp	644	63.5	5.2	741	2	S73827	cyclic nucleotide
572	64	5.3	445	2	A70732	hypothetical prote	645	63.5	5.2	771	2	T50299	hypothetical serin
573	64	5.3	447	2	T13204	hypothetical prote	646	63.5	5.2	776	2	T20896	hypothetical prote
574	64	5.3	457	2	T39751	major facilitator	647	63.5	5.2	845	2	D97163	cation transport p
575	64	5.3	461	2	T11800	NMDH2 dehydrogenas	648	63.5	5.2	845	2	D97163	hypothetical prote
576	64	5.3	466	2	G71542	probable amino aci	649	63.5	5.2	1050	2	AE0380	multidrug efflux p
577	64	5.3	470	2	AD1430	transmembrane effl	650	63.5	5.2	1103	2	T42022	probable chitin su
578	64	5.3	492	2	S59107	NMDH2 dehydrogenas	651	63.5	5.2	1120	2	S59359	GNMVP
579	64	5.3	565	2	T16408	hypothetical prote	652	63.5	5.2	1240	2	S64916	probable membrane
580	64	5.3	692	2	E90113	hypothetical prote	653	63.5	5.2	1604	2	B86287	Fcγ1.23 protein -
581	64	5.3	768	2	T22758	hypothetical prote	654	63.5	5.2	1612	2	S51243	probable ATPase (E
582	64	5.3	798	2	T23539	hypothetical prote	655	63.5	5.2	2143	2	JH0427	voltage-dependent
583	64	5.3	810	2	T33323	hypothetical prote	656	63.5	5.2	3388	1	G97022	genome polyprotein
584	64	5.3	953	2	T01093	lumidependens pr	657	63.5	5.2	115	2	G97022	probable membrane
585	64	5.3	970	2	F64230	spore germination	658	63	5.2	134	2	S40376	Ig kappa chain - h
586	64	5.3	992	2	A42318	glycogen phosphory	659	63	5.2	217	2	F83840	stage II sporulati
587	64	5.3	996	2	A95228	bacteriocin format	660	63	5.2	218	1	A40181	23K integral membr
588	64	5.3	996	2	E98092	cylM protein, cyto	661	63	5.2	232	2	B90129	26S proteasome SU
589	64	5.3	1174	2	A39927	RNA-directed RNA p	662	63	5.2	239	2	S66341	ribonuclease I (EC
590	64	5.3	1182	2	T13952	membrane protein p	663	63	5.2	239	2	F64382	hypothetical prote
591	64	5.3	1280	2	A39117	170K lectin precu	664	63	5.2	251	2	E90658	conserved hypotet
592	64	5.3	1297	2	T39287	hypothetical prote	665	63	5.2	254	2	E90657	hypothetical prote
593	64	5.3	1689	2	S72467	sodium channel pro	666	63	5.2	254	2	E85488	hypothetical prote
594	64	5.3	2787	2	S45416	TEII protein - Yea	667	63	5.2	257	2	A32283	MHC class II hist
595	63.5	5.2	115	2	AB2223	hypothetical prote	668	63	5.2	260	2	A34178	MHC class II hist
596	63.5	5.2	145	2	AB2280	hypothetical prote	669	63	5.2	271	2	AC1320	bacteriorhodopsin
597	63.5	5.2	158	2	I61900	eosinophil-derived	670	63	5.2	276	2	F72342	hypothetical prote
598	63.5	5.2	171	2	I48085	integral membrane	671	63	5.2	292	2	T19669	conserved hypotet
599	63.5	5.2	219	2	I45937	MHC cell surface g	672	63	5.2	292	2	G88783	protein C33A12.16
600	63.5	5.2	253	2	S20737	chitinase (EC 3.2.	673	63	5.2	295	2	A41241	ubiquitin-conjugat
601	63.5	5.2	253	2	S20738	chitinase (EC 3.2.	674	63	5.2	309	2	AC0489	probable membrane
602	63.5	5.2	261	1	HLH01C	MHC class II histo	675	63	5.2	313	2	S66962	probable membrane
603	63.5	5.2	261	2	I55996	MHC HLA-DQ-beta	676	63	5.2	314	2	T33862	hypothetical prote
604	63.5	5.2	261	2	B37044	MHC class II histo	677	63	5.2	320	2	T26259	hypothetical prote
605	63.5	5.2	261	2	I54480	MHC class II histo	678	63	5.2	339	2	A81288	probable sugar kin
606	63.5	5.2	261	2	I68732	HLA DQ-beta - huma	679	63	5.2	341	2	S63666	platelet activatin
607	63.5	5.2	263	2	I45943	MHC class II - bov	680	63	5.2	341	2	AE1824	permease protein o
608	63.5	5.2	263	2	T46093	hypothetical prote	681	63	5.2	353	2	A88987	protein C50H11.4 [
609	63.5	5.2	273	2	T49007	hypothetical prote	682	63	5.2	354	2	T20169	hypothetical prote
610	63.5	5.2	275	2	D65100	hypothetical L-ser	683	63	5.2	356	2	G82938	hemin transport sy
611	63.5	5.2	286	2	A13105	hypothetical prote	684	63	5.2	360	2	F70819	probable ionictan
612	63.5	5.2	288	2	A90135	SAM-dependent meth	685	63	5.2	376	2	S33654	zinc transport pro
613	63.5	5.2	301	2	C98181	sItC protein (AF12	686	63	5.2	379	2	S58464	ubiquinol-cytochro

687	63	5.2	391	2	H88955	protein K04F1.2 [i	760	62.5	5.1	466	2	T32204	hypothetical prote
688	63	5.2	394	2	AC1554	D1b protein for D	470	62.5	5.1	470	2	G97263	PTS system enzyme
689	63	5.2	400	2	F86887	hypothetical prote	762	62.5	5.1	473	2	G90401	.flaegella-related p
690	63	5.2	418	2	E86395	hypothetical prote	763	62.5	5.1	481	2	T23131	hypothetical prote
691	63	5.2	429	2	AC0801	probable amino aci	764	62.5	5.1	497	2	F86712	di-/tripeptide tra
692	63	5.2	430	2	A90313	transport protein	765	62.5	5.1	502	2	T05135	hypothetical prote
693	63	5.2	433	2	AF1739	PTS system, celllob	766	62.5	5.1	505	2	AD0511	probable carnitine
694	63	5.2	434	2	T19205	hypothetical prote	767	62.5	5.1	516	2	A84081	hypothetical prote
695	63	5.2	437	2	H81041	citrate transport	768	62.5	5.1	522	2	T18504	hypothetical prote
696	63	5.2	438	2	A64147	hypothetical prote	769	62.5	5.1	546	2	D83408	hypothetical prote
697	63	5.2	440	2	T24837	hypothetical prote	770	62.5	5.1	548	2	T47510	probable transport
698	63	5.2	440	2	JS0616	serotonin receptor	771	62.5	5.1	617	2	T51917	related to transfo
699	63	5.2	458	2	AF0771	probable transport	772	62.5	5.1	638	2	S36546	El protein - human
700	63	5.2	470	2	C97853	NADH2 dehydrogenas	773	62.5	5.1	657	2	AS4011	cationic amino aci
701	63	5.2	494	2	B33531	cytochrome P450 2A	774	62.5	5.1	657	2	S37592	beta-fructofuranos
702	63	5.2	494	2	T15322	hypothetical prote	775	62.5	5.1	698	2	T12161	NADH2 dehydrogenas
703	63	5.2	521	2	C71315	hypothetical prote	776	62.5	5.1	700	2	T12162	NADH2 dehydrogenas
704	63	5.2	526	2	C71315	probable virulence	777	62.5	5.1	711	2	D86296	hypothetical prote
705	63	5.2	532	2	T23481	hypothetical prote	778	62.5	5.1	715	2	B83222	regulatory protein
706	63	5.2	533	2	H86282	protein F10B6.34 [779	62.5	5.1	718	2	A89195	hypothetical prote
707	63	5.2	556	2	S51892	probable membrane	780	62.5	5.1	849	2	T02186	probable RNA-bind
708	63	5.2	567	2	S58750	NADH2 dehydrogenas	781	62.5	5.1	855	1	J02003	env polyprotein -
709	63	5.2	600	2	T11889	laccase (EC 1.10.3	782	62.5	5.1	1021	2	A28199	Na+/K+-exchanging
710	63	5.2	619	1	KSNCTO	laccase (EC 1.10.3	783	62.5	5.1	1070	2	F90106	IAP100 protein [im
711	63	5.2	619	1	KSNCTT	probable membrane	784	62.5	5.1	1079	2	I59362	calcium/polyvalent
712	63	5.2	651	2	AG0448	semaphorin homolog	785	62.5	5.1	1083	2	S76111	acrilflavin resista
713	63	5.2	653	2	T03102	sulfate transport	786	62.5	5.1	1242	2	G88480	protein C16A3.7 [i
714	63	5.2	662	2	S51764	structural protein	787	62.5	5.1	1289	2	S69689	hypothetical prote
715	63	5.2	681	2	S33316	probable copper-tr	788	62.5	5.1	1523	2	T13953	MEGF2, protein - ra
716	63	5.2	745	1	S75354	gene COX1, intron 4	789	62.5	5.1	1560	2	T00080	hypothetical poly
717	63	5.2	763	2	S17998	gene 51 protein -	790	62.5	5.1	1811	2	T00035	nonstructural poly
718	63	5.2	835	1	W2BE51	hypothetical prote	791	62	5.1	165	2	AG1903	hypothetical prote
719	63	5.2	870	2	T25338	respiratory burst	792	62	5.1	167	2	T15114	cytochrome-c oxida
720	63	5.2	921	2	T51804	hypothetical prote	793	62	5.1	261	2	G58888	cytochrome-c oxida
721	63	5.2	956	2	T40953	cell division cont	794	62	5.1	265	2	B97272	gamma-glutamyl hyd
722	63	5.2	974	2	S15038	probable disease r	795	62	5.1	318	2	JC6115	phosphate transpor
723	63	5.2	994	2	H96510	hypothetical prote	796	62	5.1	319	1	BVECPW	phosphate transpor
724	63	5.2	1030	2	T18669	hypothetical prote	797	62	5.1	319	2	AC0956	phosphate transpor
725	63	5.2	1043	2	F97302	opreact receptor p	798	62	5.1	319	2	G86057	probable G protein
726	63	5.2	1125	1	OYURCP	hypothetical prote	799	62	5.1	319	2	G91211	probable G protein
727	63	5.2	1194	2	E96624	hypothetical prote	800	62	5.1	320	2	S17177	ubiquitinol-cytochro
728	63	5.2	1294	2	S77690	probable membrane	801	62	5.1	324	1	C69861	hypothetical prote
729	63	5.2	1430	2	T27924	hypothetical prote	802	62	5.1	335	2	T32657	connexin40 - human
730	63	5.2	1776	1	KRWPYM	genome polypotein	803	62	5.1	358	2	I38429	hypothetical prote
731	63	5.2	1998	2	T13009	hypothetical prote	804	62	5.1	365	2	F85018	conserved hypochet
732	63	5.2	2809	2	T30213	G-cadherin - sea u	805	62	5.1	365	2	H71268	hypothetical prote
733	62.5	5.1	144	2	S21349	hydroethanol 16.3K	806	62	5.1	369	2	A72453	ubiquitinol-cytochro
734	62.5	5.1	174	1	RDSPPA	ferredoxin-chiored	807	62	5.1	379	1	S17411	hypothetical prote
735	62.5	5.1	206	2	D83317	conserved hypochet	808	62	5.1	382	1	S33573	conserved hypochet
736	62.5	5.1	207	2	AG2553	hypothetical prote	809	62	5.1	388	1	D70006	dipeptidyl peptida
737	62.5	5.1	237	2	T05249	hypothetical prote	810	62	5.1	402	2	B75297	probable tryptopha
738	62.5	5.1	249	2	E90048	hypothetical prote	811	62	5.1	414	2	A10156	hypothetical prote
739	62.5	5.1	261	1	HLHU2C	MGC class II histio	812	62	5.1	421	2	T27311	hypothetical prote
740	62.5	5.1	261	2	B32527	class II histocomp	813	62	5.1	427	2	F97790	putrescine-ornithi
741	62.5	5.1	276	2	H96965	probable hydrolase	814	62	5.1	429	2	AG3150	hypothetical prote
742	62.5	5.1	296	2	A11530	conserved hypochet	815	62	5.1	432	2	A84798	hypothetical prote
743	62.5	5.1	297	1	A30586	B-cell surface ant	816	62	5.1	433	2	S77340	hypothetical prote
744	62.5	5.1	301	2	H70584	phosphate specific	817	62	5.1	439	2	B40839	putrescine/ornithi
745	62.5	5.1	301	2	C85049	cytochrome-c oxida	818	62	5.1	439	2	H90718	putrescine transpo
746	62.5	5.1	311	2	S66600	conserved hypochet	819	62	5.1	439	2	H85568	hypothetical prote
747	62.5	5.1	326	2	G89835	hypothetical prote	820	62	5.1	444	2	T32648	hypothetical prote
748	62.5	5.1	327	2	T25780	hypothetical prote	821	62	5.1	445	2	T05887	hypothetical prote
749	62.5	5.1	350	1	K1B8EC	thymidine kinase (822	62	5.1	447	2	F75016	PTS system, IIC co
750	62.5	5.1	350	1	D97298	uncharacterized me	823	62	5.1	448	2	F95036	glucan 1,3-beta-gl
751	62.5	5.1	351	2	S29152	rhodopsin - chicke	824	62	5.1	448	2	B97907	hypothetical prote
752	62.5	5.1	394	2	S39739	efflux protein hom	825	62	5.1	448	2	JN0118	glucan 1,3-beta-gl
753	62.5	5.1	396	1	G64313	protein-export mem	826	62	5.1	450	2	A12324	NADH2 dehydrogena
754	62.5	5.1	397	2	C83470	hypothetical prote	827	62	5.1	452	2	C71391	amino acid transp
755	62.5	5.1	413	2	S29027	aspartate transami	828	62	5.1	473	2	T04965	NADH2 dehydrogena
756	62.5	5.1	416	2	E83590	cytosine permease	829	62	5.1	488	1	OXASM4	endo-1,4-beta-gluc
757	62.5	5.1	435	2	A12082	hypothetical prote	830	62	5.1	492	2	B96731	uncharacterized me
758	62.5	5.1	446	2	G72287	hypothetical prote	831	62	5.1	492	2	H97274	hypothetical prote
759	62.5	5.1	450	2	B81730	conserved hypochet	832	62	5.1	538	2	T05130	hypothetical prote

833	62	5.1	609	2	T32456	hypothetical prote	906	61.5	5.1	647	2	JQ2149	B west mating prot
834	62	5.1	610	2	T11544	NADH2 dehydrogenas	907	61.5	5.1	651	2	FB2124	cytochrome c-type
835	62	5.1	628	2	B91146	probable integral	908	61.5	5.1	661	2	S37591	beta-fructofuranos
836	62	5.1	628	2	F85991	probable integral	909	61.5	5.1	661	2	S37590	beta-fructofuranos
837	62	5.1	631	2	B98137	hypothetical 46.1K	910	61.5	5.1	670	1	DNOB05	NADH2 dehydrogenas
838	62	5.1	640	2	D70850	probable oxidoredu	911	61.5	5.1	673	1	S59263	probable membrane
839	62	5.1	646	2	JN0473	P-selectin precurs	912	61.5	5.1	677	1	A45224	system b(0,+) amin
840	62	5.1	659	2	AF3489	cytochrome c ubiqu	913	61.5	5.1	698	2	T12559	NADH2 dehydrogenas
841	62	5.1	662	2	T01857	hypothetical prote	914	61.5	5.1	699	2	T12167	NADH2 dehydrogenas
842	62	5.1	771	2	S45048	capsid protein - h	915	61.5	5.1	699	2	T12172	NADH2 dehydrogenas
843	62	5.1	826	2	T15751	hypothetical prote	916	61.5	5.1	787	2	S09411	DNA translocase sp
844	62	5.1	949	1	PXM0P1	H+-exporting ATPas	917	61.5	5.1	799	2	T48451	myotubularin-like
845	62	5.1	972	2	E97421	NADH dehydrogenase	918	61.5	5.1	839	2	JC6015	chitin synthase (E
846	62	5.1	994	2	AD2639	pH adaptation potass	919	61.5	5.1	898	2	D86122	Mg(2+) transport ATP
847	62	5.1	1083	2	T05689	hypothetical prote	920	61.5	5.1	898	2	E65236	Mg(2+) transport ATP
848	62	5.1	1166	2	T13958	synGAP-b1 protein	921	61.5	5.1	898	2	C91281	Mg(2+) transport ATP
849	62	5.1	1249	2	T14270	Ras-GTPase activat	922	61.5	5.1	929	2	C90531	cation-transportin
850	62	5.1	1293	2	T14259	ras GTPase-activat	923	61.5	5.1	972	2	S67048	MTRIO protein - ye
851	62	5.1	2139	2	A44467	voltage-dependent	924	61.5	5.1	1029	2	AG3363	acriiflavin resista
852	62	5.1	3119	2	I49729	HD protein - mouse	925	61.5	5.1	1034	2	S49947	SMT4 protein - yea
853	61.5	5.1	115	2	A23329	ly-5-8 glycoprotei	926	61.5	5.1	1344	2	S47412	gene P2 protein -
854	61.5	5.1	161	2	I37034	ectinophil-derived	927	61.5	5.1	1449	2	S47423	E2 glycoprotein pr
855	61.5	5.1	222	2	T27916	hypothetical prote	928	61.5	5.1	1488	2	F86428	probable ABC trans
856	61.5	5.1	238	2	T23352	hypothetical prote	929	61.5	5.1	2179	1	GNNYH4	genome polypotein
857	61.5	5.1	248	2	S76774	thiol-disulfide in	930	61.5	5.0	155	2	G90043	hypothetical prote
858	61.5	5.1	257	2	AC1290	hypothetical prote	931	61.5	5.0	189	2	A71569	hypothetical prote
859	61.5	5.1	260	2	I45939	MHC cell surface g	932	61.5	5.0	193	2	B91170	hypothetical membr
860	61.5	5.1	268	2	D29312	MHC class II histo	933	61.5	5.0	193	2	B86016	hypothetical prote
861	61.5	5.1	272	2	T09132	26S proteasome bet	934	61.5	5.0	200	2	S43593	hypothetical prote
862	61.5	5.1	281	2	C69504	probable heme A fa	935	61.5	5.0	213	2	A34633	M04D8.6 protein -
863	61.5	5.1	301	1	S10456	cytochrome c-type	936	61.5	5.0	216	2	C87037	H+-exporting ATPas
864	61.5	5.1	325	1	B40358	NADH2 dehydrogenas	937	61.5	5.0	226	2	I49589	probable secreted
865	61.5	5.1	325	1	DNMTU1	NADH2 dehydrogenas	938	61.5	5.0	251	2	T44070	antigen - mouse
866	61.5	5.1	325	1	S49576	NADH2 dehydrogenas	939	61.5	5.0	255	2	E64604	conserved hypochet
867	61.5	5.1	325	1	T32282	hypothetical prote	940	61.5	5.0	257	2	E54285	conserved hypochet
868	61.5	5.1	336	2	S75437	hypothetical prote	941	61.5	5.0	274	2	C47700	MHC class II histo
869	61.5	5.1	355	2	S14686	geranylgeranyltran	942	61.5	5.0	282	2	T03906	glycerol uptake fa
870	61.5	5.1	362	2	A39714	G protein-coupled	943	61.5	5.0	287	2	C82158	cytochrome B561 ho
871	61.5	5.1	371	1	A75033	probable hexoxyltr	944	61.5	5.0	287	2	D83438	ROK family protein
872	61.5	5.1	377	2	G90737	hypothetical prote	945	61.5	5.0	302	2	T03109	probable membrane
873	61.5	5.1	377	2	H85587	hypothetical prote	946	61.5	5.0	302	2	E64311	probable membrane
874	61.5	5.1	377	2	A64816	yhbs protein - Esc	947	61.5	5.0	316	2	E83768	Na+/Ca2+-exchangin
875	61.5	5.1	385	2	I51307	basolateral Na(+)-	948	61.5	5.0	322	2	D96921	D-3-phosphoglycera
876	61.5	5.1	391	2	AB1285	transmembrane tran	949	61.5	5.0	326	2	S70596	oligopeptide trans
877	61.5	5.1	394	2	S23481	benz protein - Aci	950	61.5	5.0	348	2	T04923	NADH2 dehydrogenas
878	61.5	5.1	397	2	AF3285	membrane protein m	951	61.5	5.0	369	2	S74017	hypothetical prote
879	61.5	5.1	417	2	AG1934	folylipolyglutamate	952	61.5	5.0	375	2	C97217	GDEF domain conta
880	61.5	5.1	444	2	D97142	surface-layer rela	953	61.5	5.0	379	1	S17417	ubiquinol-cytochro
881	61.5	5.1	461	2	T11819	glycerol-3-phospha	954	61.5	5.0	379	1	A41833	ubiquinol-cytochro
882	61.5	5.1	462	2	D26488	tubulin alpha-4 ch	955	61.5	5.0	379	2	T48135	ubiquinol-cytochro
883	61.5	5.1	468	2	T41284	hypothetical prote	956	61.5	5.0	379	2	T11401	ubiquinol-cytochro
884	61.5	5.1	472	2	E81784	glutamate-ammonia	957	61.5	5.0	380	2	T11603	ubiquinol-cytochro
885	61.5	5.1	481	2	T27435	hypothetical prote	958	61.5	5.0	382	2	S73256	hypothetical prote
886	61.5	5.1	487	2	T49424	hypothetical prote	959	61.5	5.0	392	2	E91290	probable transport
887	61.5	5.1	491	2	B86096	xylose-proton sym	960	61.5	5.0	392	2	H86131	probable transport
888	61.5	5.1	491	2	F91255	xylose-proton sym	961	61.5	5.0	401	2	H69833	conserved hypochet
889	61.5	5.1	491	2	A26430	xylose transport p	962	61.5	5.0	402	2	G89911	conserved hypochet
890	61.5	5.1	497	1	WMBELM	membrane protein L	963	61.5	5.0	412	2	S13035	aspartate transami
891	61.5	5.1	504	2	A83901	hypothetical prote	964	61.5	5.0	413	2	S29028	aspartate transami
892	61.5	5.1	510	1	DERZM2	NADH2 dehydrogenas	965	61.5	5.0	413	2	JT0439	aspartate transami
893	61.5	5.1	510	2	S65075	NADH2 dehydrogenas	966	61.5	5.0	429	2	AH2409	hypothetical prote
894	61.5	5.1	512	2	E96024	conserved hypochet	967	61.5	5.0	430	2	B83533	hypothetical prote
895	61.5	5.1	516	2	T47509	probable transport	968	61.5	5.0	445	2	B83533	hypothetical prote
896	61.5	5.1	524	2	S28902	glutamate transport	969	61.5	5.0	445	2	A121724	potassium uptake p
897	61.5	5.1	530	2	T04871	hypothetical prote	970	61.5	5.0	448	2	B83931	hypothetical prote
898	61.5	5.1	533	2	E64626	ABC transporter, A	971	61.5	5.0	460	1	S40439	allantoin alpha-2 ch
899	61.5	5.1	533	2	H71886	probable ABC trans	972	61.5	5.0	463	2	S48489	allantoinase (EC 3
900	61.5	5.1	537	2	T02982	probable sucrose t	973	61.5	5.0	463	2	G85781	part of a kinase (
901	61.5	5.1	538	2	E72752	hypothetical prote	974	61.5	5.0	463	2	C90933	part of a kinase (
902	61.5	5.1	543	2	S65462	glucose transport	975	61.5	5.0	466	2	S36577	l2 protein - human
903	61.5	5.1	547	2	D95337	glucose transport	976	61.5	5.0	467	2	S33181	glutamate-ammonia
904	61.5	5.1	575	2	D71642	glutathione-regula	977	61.5	5.0	475	2	T33943	hypothetical prote
905	61.5	5.1	611	2	T21747	hypothetical prote	978	61.5	5.0	480	2	S50525	hypothetical prote
										485	2	E97506	potassium uptake p

1125	60	4.9	228	1	A40402	CD9 antigen [valid	1198	60	4.9	502	2	E87596	tryptophan halogen
1126	60	4.9	228	1	A42929	CD9 antigen - gree	1199	60	4.9	508	2	T19350	hypothetical prote
1127	60	4.9	228	2	B90369	hypothetical prote	1200	60	4.9	509	2	A32101	glucose transport
1128	60	4.9	234	2	AG1220	glycerol uptake fa	1201	60	4.9	534	2	C84811	phosphate transpor
1129	60	4.9	251	2	H69441	carboxylesterase (1202	60	4.9	556	2	H82287	malate synthase A
1130	60	4.9	257	2	A11661	hypothetical prote	1203	60	4.9	557	2	AB0204	methvl-accepting c
1131	60	4.9	258	2	154458	MHC class II histo	1204	60	4.9	557	2	T46520	probable transmemb
1132	60	4.9	265	2	A83969	hypothetical prote	1205	60	4.9	557	2	S58688	probable transpor
1133	60	4.9	268	2	T24795	hypothetical prote	1206	60	4.9	577	2	T32336	hypothetical prote
1134	60	4.9	287	2	T18735	hypothetical prote	1207	60	4.9	578	2	T35537	cytochrome-c oxida
1135	60	4.9	291	2	E91089	prolipoprotein dia	1208	60	4.9	603	2	H69121	hypothetical prote
1136	60	4.9	291	2	C85934	prolipoprotein dia	1209	60	4.9	608	2	T25572	hypothetical prote
1137	60	4.9	291	2	A56149	prolipoprotein dia	1210	60	4.9	616	2	A30304	prolactin receptor
1138	60	4.9	293	2	AF2904	ABC transporter, m	1211	60	4.9	623	2	C86184	hypothetical prote
1139	60	4.9	293	2	H97679	probable ABC trans	1212	60	4.9	633	2	S45877	uracil transport p
1140	60	4.9	301	2	S76574	hypothetical prote	1213	60	4.9	635	2	S30018	allantoin transport
1141	60	4.9	303	2	AE3129	conserved hypothec	1214	60	4.9	638	2	T11801	NADH2 dehydrogenas
1142	60	4.9	303	2	D98158	hypothetical prote	1215	60	4.9	640	2	S23008	insulin-like growt
1143	60	4.9	307	2	G84962	hypothetical prote	1216	60	4.9	679	2	A83488	hypothetical prote
1144	60	4.9	309	2	T40759	synaptaxin, vesicula	1217	60	4.9	703	2	T13074	NADH2 dehydrogenas
1145	60	4.9	338	2	G70584	phosphate transpor	1218	60	4.9	746	1	HYH1MA	meprin A (EC 3.4.2
1146	60	4.9	348	2	E86818	dehydrogenase (imp	1219	60	4.9	795	2	T31180	hypothetical prote
1147	60	4.9	350	2	B82281	ferric vibriobactri	1220	60	4.9	795	2	H70934	hypothetical prote
1148	60	4.9	355	2	151319	Rh2 opsin - green	1221	60	4.9	860	2	T49910	hypothetical prote
1149	60	4.9	357	2	T33237	hypothetical prote	1222	60	4.9	933	2	T49910	probable NADH dehy
1150	60	4.9	365	2	138748	prostaglandin recep	1223	60	4.9	960	2	T06688	H ⁺ -exporting Arpas
1151	60	4.9	365	2	S51315	prostaglandin E re	1224	60	4.9	975	2	T16073	hypothetical prote
1152	60	4.9	370	2	H90559	hypothetical prote	1225	60	4.9	1033	2	T49179	Ca2+-transporting
1153	60	4.9	374	2	I38747	prostaglandin recep	1226	60	4.9	1095	2	A54145	sodium-potassium-c
1154	60	4.9	374	2	S51317	prostaglandin E re	1227	60	4.9	1128	2	T04922	hypothetical prote
1155	60	4.9	374	2	T26200	hypothetical prote	1228	60	4.9	1307	2	T25106	hypothetical prote
1156	60	4.9	379	1	S41834	ubiquinol-cytochro	1229	60	4.9	1402	2	T24664	hypothetical prote
1157	60	4.9	379	1	S43267	ubiquinol-cytochro	1230	60	4.9	1487	2	G96827	protein P20B17.10
1158	60	4.9	379	2	S58450	ubiquinol-cytochro	1231	60	4.9	1492	2	T18560	DNA-directed DNA p
1159	60	4.9	379	2	AE3225	ABC transporter, m	1232	60	4.9	1532	2	S48933	probable transport
1160	60	4.9	380	2	EU0053	unpuglucose-hexose-	1233	60	4.9	1945	2	T113937	plexin A - fruit f
1161	60	4.9	380	2	EB1302	probable type I re	1234	60	4.9	2090	2	T30075	hypothetical prote
1162	60	4.9	381	2	T11440	ubiquinol-cytochro	1235	60	4.9	2153	2	T30074	hypothetical prote
1163	60	4.9	381	2	T23250	hypothetical prote	1236	60	4.9	2201	2	AH0095	probable sideropho
1164	60	4.9	382	2	G90751	probable transport	1237	60	4.9	2476	2	T34022	zomadesin - pig
1165	60	4.9	382	2	E85615	probable transp	1238	60	4.9	3144	2	A46068	Huntington disease
1166	60	4.9	382	2	A64829	membrane protein y	1239	59.5	4.9	88	2	G82754	hypothetical prote
1167	60	4.9	388	2	S51316	prostaglandin recep	1240	59.5	4.9	92	2	D43674	u55 protein - huma
1168	60	4.9	388	2	I38750	prostaglandin recep	1241	59.5	4.9	112	2	A46717	collase precursor
1169	60	4.9	390	2	S43375	prostaglandin E re	1242	59.5	4.9	128	2	S40379	ig kappa chain V-J
1170	60	4.9	390	2	S51313	prostaglandin E re	1243	59.5	4.9	150	2	C86876	hypothetical prote
1171	60	4.9	393	2	AC2782	diaminoptemilate de	1244	59.5	4.9	155	2	D72761	hypothetical prote
1172	60	4.9	393	2	S51318	prostaglandin B re	1245	59.5	4.9	161	2	A33922	eosinophil-derived
1173	60	4.9	393	2	E96954	Na/H antiporter (n	1246	59.5	4.9	198	1	A60620	prolactin - green
1174	60	4.9	394	2	AE1196	DLTB protein for D	1247	59.5	4.9	204	2	A10059	probable lyse type
1175	60	4.9	400	2	AG0068	cell division prot	1248	59.5	4.9	227	2	H90109	27.2K hypothetical
1176	60	4.9	403	2	G64427	hypothetical prote	1249	59.5	4.9	234	2	AB1574	glycerol uptake fa
1177	60	4.9	405	2	AE1474	probable permeases	1250	59.5	4.9	234	2	AB1574	late expression fa
1178	60	4.9	412	2	S72579	hypothetical prote	1251	59.5	4.9	235	2	T30473	RhtB family transp
1179	60	4.9	417	2	A45794	tubulin alpha chai	1252	59.5	4.9	235	2	E97679	hypothetical prote
1180	60	4.9	422	2	AB3635	probable O-antigen	1253	59.5	4.9	235	2	G64810	hypothetical prote
1181	60	4.9	425	2	S51319	prostaglandin E re	1254	59.5	4.9	242	2	A69026	pnuic proteain - Bsc
1182	60	4.9	436	2	AC1021	proton glutamate s	1255	59.5	4.9	244	2	B83142	conserved hypothec
1183	60	4.9	437	2	UC3459	inulin fructotrans s	1256	59.5	4.9	255	2	D71910	hypothetical prote
1184	60	4.9	440	2	D97561	DNK (AB033991) [i	1257	59.5	4.9	261	2	S68134	cytochrome-c oxida
1185	60	4.9	449	2	C75053	DNA damage-inducib	1258	59.5	4.9	263	2	S72528	cytochrome-c oxida
1186	60	4.9	452	2	F64730	UDP-N-acetylmutamo	1259	59.5	4.9	270	2	AF2008	chitinase (EC 3.2.
1187	60	4.9	455	2	T37517	hypothetical prote	1260	59.5	4.9	287	2	A25877	permease protein o
1188	60	4.9	458	2	B81409	probable transmemb	1261	59.5	4.9	289	2	H86880	cytochrome-c oxida
1189	60	4.9	462	2	D81251	NADH2 dehydrogenas	1262	59.5	4.9	291	2	S73242	transporter yvvd [
1190	60	4.9	463	2	S59968	secy protein - Sul	1263	59.5	4.9	293	1	Q08BG1	hypothetical prote
1191	60	4.9	465	2	H87627	response regulator	1264	59.5	4.9	307	2	B82394	HVLF1 protein - hu
1192	60	4.9	469	2	AE3374	glutamate-ammonia	1265	59.5	4.9	309	2	T31908	hypothetical prote
1193	60	4.9	474	2	T34193	G protein-coupled	1266	59.5	4.9	310	2	S64619	hypothetical prote
1194	60	4.9	476	2	H82085	sodium/alanine sym	1267	59.5	4.9	318	2	AB0350	probable membrane
1195	60	4.9	478	2	A37430	calcitonin recepto	1268	59.5	4.9	321	2	T45986	hypothetical prote
1196	60	4.9	479	2	S33746	calcitonin recepto	1269	59.5	4.9	324	2	H86533	integral membrane
1197	60	4.9	491	2	G84498	hypothetical prote	1270	59.5	4.9	344	2	H72088	ABC transporter, p

1271	59.5	4.9	327	2	G88976	protein F54E2.6 [1	1344	59.5	4.9	615	2	H82635	hypothetical prote
1272	59.5	4.9	328	2	T11938	NADH2 dehydrogenas	1345	59.5	4.9	622	2	B71326	probable V-type AT
1273	59.5	4.9	329	2	H83907	cytochrome aa3 qui	1346	59.5	4.9	626	2	B71326	conserved hypothet
1274	59.5	4.9	336	2	AC2413	hypothetical prote	1347	59.5	4.9	633	2	T13306	hypothetical prote
1275	59.5	4.9	337	2	AC2413	effector cell prot	1348	59.5	4.9	633	2	T48902	sulfate transporte
1276	59.5	4.9	341	2	F82301	peptide ABC transp	1349	59.5	4.9	658	2	T49069	sulfate transporte
1277	59.5	4.9	343	2	D83282	probable permease	1350	59.5	4.9	658	2	T48901	sulfate transporte
1278	59.5	4.9	343	2	D83282	hypothetical prote	1351	59.5	4.9	660	2	H87590	cytochrome c-type
1279	59.5	4.9	345	2	AD2998	transporter Atu351	1352	59.5	4.9	682	2	T18847	hypothetical prote
1280	59.5	4.9	345	2	E98285	YrkH (A010131) [1	1353	59.5	4.9	686	2	A45483	chloride channel,
1281	59.5	4.9	353	1	D65025	probable permease	1354	59.5	4.9	699	2	T12170	NADH2 dehydrogenas
1282	59.5	4.9	353	2	G85892	probable permease	1355	59.5	4.9	699	2	T12173	NADH2 dehydrogenas
1283	59.5	4.9	353	2	C91048	probable permease	1356	59.5	4.9	703	2	T51161	hypothetical prote
1284	59.5	4.9	355	2	T32723	hypothetical prote	1357	59.5	4.9	710	2	S62575	hypothetical prote
1285	59.5	4.9	366	2	T50468	probable maturase	1358	59.5	4.9	714	2	S76082	hypothetical prote
1286	59.5	4.9	376	2	A86382	43 kR hypothetical	1359	59.5	4.9	726	2	S22258	probable protein k
1287	59.5	4.9	379	1	S41847	ubiquinol-cytochro	1360	59.5	4.9	778	2	T05341	S-receptor kinase
1288	59.5	4.9	379	1	S58454	ubiquinol-cytochro	1361	59.5	4.9	800	2	G89831	hypothetical prote
1289	59.5	4.9	379	1	H82284	queuine tRNA-ribos	1362	59.5	4.9	821	2	T41364	hypothetical prote
1290	59.5	4.9	387	2	T31748	glycerol-3-phospha	1363	59.5	4.9	828	2	E71417	iodide peroxidase
1291	59.5	4.9	396	2	S01660	hypothetical prote	1364	59.5	4.9	914	1	UN0550	probable membrane
1292	59.5	4.9	396	2	T39337	hypothetical prote	1365	59.5	4.9	953	2	S19427	probable membrane
1293	59.5	4.9	402	2	AG0638	probable membrane	1366	59.5	4.9	1027	2	T43024	ceob protein - Bur
1294	59.5	4.9	410	2	E75048	multidrug resistan	1367	59.5	4.9	1068	2	T41671	hypothetical prote
1295	59.5	4.9	410	2	D71897	hypothetical prote	1368	59.5	4.9	1129	2	D84022	ATP-dependent nucl
1296	59.5	4.9	418	2	G70864	probable transemb	1369	59.5	4.9	1161	2	B70544	DNA polymerase III
1297	59.5	4.9	428	2	T25950	hypothetical prote	1370	59.5	4.9	1187	2	T20544	hypothetical prote
1298	59.5	4.9	430	2	T12541	hypothetical prote	1371	59.5	4.9	1217	2	T13996	pol protein - fru1
1299	59.5	4.9	431	1	SAVDC2	large surface anti	1372	59.5	4.9	1230	2	T18291	patched protein -
1300	59.5	4.9	433	1	T17654	hypothetical prote	1373	59.5	4.9	1237	2	A54080	protein-tyrosine-p
1301	59.5	4.9	433	2	T27731	hypothetical prote	1374	59.5	4.9	1247	2	T18671	hypothetical prote
1302	59.5	4.9	437	2	A36372	membrane transpor	1375	59.5	4.9	1268	2	G85154	hypothetical prote
1303	59.5	4.9	440	2	T11319	NADH2 dehydrogenas	1376	59.5	4.9	1289	1	GUNBPT4	proximal tail fibe
1304	59.5	4.9	441	2	S47049	1-aminocyclopropan	1377	59.5	4.9	1429	2	T19422	hypothetical prote
1305	59.5	4.9	445	2	T42366	L-aminoadipate-sem	1378	59.5	4.9	1584	2	T18276	protein-tyrosine k
1306	59.5	4.9	449	2	A48466	tubulin alpha chai	1379	59.5	4.9	1758	2	F08559	protein-C48B4.4b [
1307	59.5	4.9	457	2	T15271	hypothetical prote	1380	59.5	4.9	1807	2	UC6319	integrin beta-4 ch
1308	59.5	4.9	465	2	S03325	transforming prote	1381	59.5	4.9	1964	2	T09059	ataxia telangiecta
1309	59.5	4.9	466	2	T41125	glucose-riigered	1382	59.5	4.9	2514	2	T37320	hypothetical prote
1310	59.5	4.9	469	2	AC3584	methylomycin a r	1383	59.5	4.9	2619	2	T24588	hypothetical prote
1311	59.5	4.9	476	2	H96802	probable amino aci	1384	59.5	4.9	3766	2	T29165	hypothetical prote
1312	59.5	4.9	479	2	T47415	transporter-like p	1385	59.5	4.9	3944	2	T19997	hypothetical prote
1313	59.5	4.9	483	2	H97246	UDP-N-acetylmuramy	1386	59.5	4.9	135	2	T49512	hypothetical prote
1314	59.5	4.9	483	2	I55598	diabetes-associated	1387	59.5	4.9	158	2	A11184	hypothetical prote
1315	59.5	4.9	485	1	KIBYHA	hexokinase (EC 2.7	1388	59.5	4.9	208	2	T05859	hypothetical prote
1316	59.5	4.9	497	2	T41015	proline rich prote	1389	59.5	4.9	208	2	A89773	hypothetical prote
1317	59.5	4.9	499	1	S30007	probable UDP-gluco	1390	59.5	4.9	219	2	D90448	conserved hypothet
1318	59.5	4.9	513	2	A81850	probable integral	1391	59.5	4.9	226	2	S57521	probable arenetical
1319	59.5	4.9	514	2	E86738	multidrug resistan	1392	59.5	4.9	242	2	S60143	cellulase (EC 3.2.
1320	59.5	4.9	520	1	A42209	D-sterespecific a	1393	59.5	4.9	248	2	T01080	hypothetical prote
1321	59.5	4.9	520	2	T20007	hypothetical prote	1394	59.5	4.9	249	2	T25643	hypothetical prote
1322	59.5	4.9	525	2	T24647	hypothetical prote	1395	59.5	4.9	250	2	B64417	hypothetical prote
1323	59.5	4.9	530	2	AG3622	rtin protein [impor	1396	59.5	4.9	254	2	B90421	hypothetical prote
1324	59.5	4.9	535	2	AG3515	hypothetical prote	1397	59.5	4.9	258	2	T59621	HLA-DPB1 - human
1325	59.5	4.9	535	2	B98022	hypothetical prote	1398	59.5	4.9	265	2	H90868	probable pump prot
1326	59.5	4.9	541	2	T31554	conserved hypothet	1399	59.5	4.9	265	2	A85750	probable pump prot
1327	59.5	4.9	541	2	D97930	hypothetical prote	1400	59.5	4.9	277	2	AE1831	hypothetical prote
1328	59.5	4.9	546	2	T23930	oligopeptide trans	1401	59.5	4.9	281	2	A10461	sn-glycerol-3-phos
1329	59.5	4.9	552	2	T51439	hypothetical prote	1402	59.5	4.9	284	2	T06129	zinc finger protei
1330	59.5	4.9	557	1	S76051	hypothetical prote	1403	59.5	4.9	289	2	G83029	hypothetical prote
1331	59.5	4.9	567	2	H67370	major facilitator	1404	59.5	4.9	292	2	C95147	l1cB protein [impo
1332	59.5	4.9	567	2	A33974	membrane transport	1405	59.5	4.9	305	2	E83890	sugar: transport by
1333	59.5	4.9	574	2	T14162	membrane transport	1406	59.5	4.9	307	2	H71160	hypothetical prote
1334	59.5	4.9	576	2	T41407	membrane transport	1407	59.5	4.9	310	2	A29884	prolactin receptor
1335	59.5	4.9	577	1	G46328	hemagglutinin-neur	1408	59.5	4.9	311	2	T32776	NADH: dehydrogenas
1336	59.5	4.9	577	1	D46328	hemagglutinin-neur	1409	59.5	4.9	313	2	S06214	NADH: dehydrogenas
1337	59.5	4.9	577	1	HNNZNC	hemagglutinin-neur	1410	59.5	4.9	322	2	H96994	coba:amin biosynth
1338	59.5	4.9	577	2	H81355	probable integral	1411	59.5	4.9	325	2	AH0796	NADH2 dehydrogenas
1339	59.5	4.9	586	2	A95167	ABC transporter, A	1412	59.5	4.9	326	2	S59101	NADH2 dehydrogenas
1340	59.5	4.9	601	2	T48539	probable potassiu	1413	59.5	4.9	329	2	AC1718	ferr:chrome ABC tr
1341	59.5	4.9	605	2	T11111	NADH2 dehydrogenas	1414	59.5	4.9	336	2	AP1378	B. subtilis ferric
1342	59.5	4.9	607	1	QXMS5M	NADH2 dehydrogenas	1415	59.5	4.9	336	2	AG1747	B. subtilis ferric
1343	59.5	4.9	612	2	A97935	hypothetical prote	1416	59.5	4.9	336	2	AG1747	

1417	59	4.9	343	2	A43577	regulatory protein
1418	59	4.9	345	2	C45456	NMDH2 dehydrogenas
1419	59	4.9	346	2	T46914	hypothetical prote
1420	59	4.9	346	2	S49959	probable membrane
1421	59	4.9	348	1	COBO	rhodopsin - bovine
1422	59	4.9	349	2	AG3010	hypothetical prote
1423	59	4.9	349	2	G98273	iron(III) dicitrat
1424	59	4.9	351	2	S14203	NMDH2 dehydrogenas
1425	59	4.9	353	2	C72479	hypothetical prote
1426	59	4.9	356	2	AE2729	cytochrome oxidase
1427	59	4.9	360	2	D84646	hypothetical prote
1428	59	4.9	361	2	T34159	hypothetical prote
1429	59	4.9	363	2	B86229	hypothetical prote
1430	59	4.9	366	2	G95376	conserved hypot
1431	59	4.9	372	2	P97510	BA483f11.2.1 (cox1
1432	59	4.9	378	2	T15816	hypothetical prote
1433	59	4.9	379	2	T11453	ubiquinol-cytochro
1434	59	4.9	382	2	T11869	ubiquinol-cytochro
1435	59	4.9	382	2	D58930	hypothetical prote
1436	59	4.9	385	2	G72638	hypothetical prote
1437	59	4.9	386	2	A26017	patatin T5 precurs
1438	59	4.9	387	2	E83679	multidrug-efflux t
1439	59	4.9	388	2	AC2011	hypothetical prote
1440	59	4.9	394	2	AB3073	tetracycline resis
1441	59	4.9	394	2	G98213	drug efflux protei
1442	59	4.9	395	2	E90896	probable transport
1443	59	4.9	395	2	B85721	probable transport
1444	59	4.9	395	2	E90677	hypothetical prote
1445	59	4.9	401	2	S42583	phosphate transloc
1446	59	4.9	403	2	F83092	probable cytochrom
1447	59	4.9	404	2	S03638	triase phosphate/3
1448	59	4.9	408	2	G69819	Na+/H+ antiporter
1449	59	4.9	412	2	A26341	aspartate transami
1450	59	4.9	412	2	T34138	hypothetical prote
1451	59	4.9	412	2	A41070	prolactin receptor
1452	59	4.9	414	2	D82487	multidrug resistan
1453	59	4.9	414	2	S39530	poly(3)-hydroxybuty
1454	59	4.9	415	2	D96759	probable serine ca
1455	59	4.9	418	2	E71848	probable nucleosid
1456	59	4.9	419	2	B69819	conserved hypot
1457	59	4.9	420	2	F69144	O-antigen transpor
1458	59	4.9	428	2	AB1611	probable proteinas
1459	59	4.9	432	2	C85087	hypothetical prote
1460	59	4.9	433	2	S31436	lg upsein chain -
1461	59	4.9	433	2	B84566	hypothetical prote
1462	59	4.9	437	2	S11497	branched-chain ami
1463	59	4.9	438	2	AF3215	ABC transporter, m
1464	59	4.9	444	2	T27866	hypothetical prote
1465	59	4.9	444	2	C75428	probable permease
1466	59	4.9	445	2	C69596	branched-chain ami
1467	59	4.9	448	2	T22194	hypothetical prote
1468	59	4.9	449	2	S55911	tubulin alpha-1 ch
1469	59	4.9	449	2	T21415	hypothetical prote
1470	59	4.9	457	2	T12399	NMDH2 dehydrogenas
1471	59	4.9	457	2	S18239	glycerol-3-phospha
1472	59	4.9	457	2	H64136	neurotransmitter t
1473	59	4.9	458	2	H82200	sodium/alanine sym
1474	59	4.9	461	2	T00621	hypothetical prote
1475	59	4.9	464	2	H83271	soluble pyridine n
1476	59	4.9	470	2	AB1804	transmembrane effl
1477	59	4.9	471	2	D64974	hypothetical prote
1478	59	4.9	471	2	H85834	probable transport
1479	59	4.9	471	2	E90989	probable transport
1480	59	4.9	473	2	T44709	acyl1/propionyl C
1481	59	4.9	476	2	A44170	membrane-bound rib
1482	59	4.9	487	1	QOECRS	xy1E protein - Bsc
1483	59	4.9	487	2	T19237	hypothetical prote
1484	59	4.9	493	2	I39541	cytoytic enteroto
1485	59	4.9	507	2	H75175	thymidine phosphor
1486	59	4.9	508	2	E90594	amino acid permea
1487	59	4.9	517	2	S77255	hypothetical prote
1488	59	4.9	523	2	S55677	glutamate transpo
1489	59	4.9	529	2	AF3059	cytochrome d oxida

1490	59	4.9	529	2	B98227	cytochrome d oxida
1491	59	4.9	534	1	S75101	hypothetical prote
1492	59	4.9	551	2	B64005	hypothetical prote
1493	59	4.9	552	2	B94076	hypothetical prote
1494	59	4.9	562	2	C71604	RNA helicase PEB08
1495	59	4.9	564	2	S73405	hexosephosphate tr
1496	59	4.9	581	2	B90539	hypothetical prote
1497	59	4.9	587	2	T23961	hypothetical prote
1498	59	4.9	598	2	T28238	ORF MSV077 hypoch
1499	59	4.9	603	2	S53301	H+-exporting ATPas
1500	59	4.9	610	2	A34631	lactogen receptor

ALIGNMENTS

RESULT 1

L6 surface protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Oct-1992 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C/Accession: A42926

R:Marken, J.S.; Schieven, G.L.; Hellstroem, I.; Hellstroem, K.E.; Aruffo, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 3503-3507, 1992

A>Title: Cloning and expression of the tumor-associated antigen L6.

A/Reference number: A42926; MUID:92228814; PMID:1565644

A/Accession: A42926

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-202 <MAR>

A/Cross-references: UNIPROT:P30408; GB:M90657; NID:G166803; PIDN:AAA36158.1; PID:G166804

C/Keywords: transmembrane protein

Query Match

Best Local Similarity 14.0%; Score 170; DB 2; Length 202;

Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;

QY	10	CNPSRLVLLLVGVALNPILVLSVDEDPQSNPISCFEWMFPGIIGAG-LMAIPRTM 68
DB	9	CIGHSLVGLALLCTIAAN-ILLYEPNGRTKYASENHSRFWFSGIVGGGLMLPAFVF 67
QY	69	SLVARRKAC-----CNRTGMFLSEFVITVIGALYGLMLISIOALKGPLMCNPSN 121
DB	68	IGHEQDDCCCGCHENGCKKCAMLSSVLAHLIGASGCVYVAALGLAEGPLCLDSLG- 126
QY	122	SNANCFSLKNISIDHESFNILQFNFNDSCAPTFGNKPTSNPTMASGWRASFFPDS- 180
DB	127	-----QW-----NYTFAS--TEGQLDPTST 145
QY	181	-----ENKRL-THFSVFLGLLVGLIEVLFGLSQIVYFGCLICG 220
DB	146	WSBCTEPKHIVENWVSLFSLIALGGLIEFLICLIQVINGVLGGICG 191

RESULT 2

tumor-associated antigen TW4SFS - human

C:Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: JC6544

Db 149 -----CHBPKN-IVEMWTLFSTLLAFGLIEFLICLIQVINGELKMC 190

RESULT 6

A85870

probable transport protein yfbs [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A85870

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grotbeck, E.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousteris, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85870

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-610 <STO>

A:Cross-references: GB:AE005174; NID:G12516645; PIDN:ANG57421.1; GSPDB:GN00145; UWGP:Z35

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yfbs

Query Match 7.4%; Score 90.5; DB 2; Length 610;

Best Local Similarity 30.8%; Pred. No. 2;

Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

Db 15 LVLVLL-----GVLNAIPILVSLVEEDFSQN-----PISCFEWMFPGIIGA 58

94 MLVLMILTVAGLGAFMSTGVVAIFIPVLSVANRMQTSPSRLMMPIS-----FAGLI-S 147

Qy 59 GLMAIPATWMSLTARKKACCNRTGMFLSFFS-----VITVIGALYCMILISIQALLKG 112

148 GMMTLVATPPRLVNVNSEL---REGYHGFSFVSVPGLVVLVGLIY--MLVMRFMLKG 202

Db

RESULT 7

H91025

probable transport protein ECS3176 [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: H91025

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: H91025

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-610 <HAY>

A:Cross-references: UNIPROT:P77741; GB:BA000007; PIDN:BA836599.1; PID:G13362646; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECS3176

Query Match 7.4%; Score 90.5; DB 2; Length 610;

Best Local Similarity 30.8%; Pred. No. 2;

Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

Qy 15 LVLVLL-----GVLNAIPILVSLVEEDFSQN-----PISCFEWMFPGIIGA 58

94 MLVLMILTVAGLGAFMSTGVVAIFIPVLSVANRMQTSPSRLMMPIS-----FAGLI-S 147

Qy 59 GLMAIPATWMSLTARKKACCNRTGMFLSFFS-----VITVIGALYCMILISIQALLKG 112

148 GMMTLVATPPRLVNVNSEL---REGYHGFSFVSVPGLVVLVGLIY--MLVMRFMLKG 202

Db

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: B65001

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co .A.; Rose, D.U.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B65001

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-610 <BLAT>

A:Cross-references: UNIPROT:P77741; GB:AE000318; GB:U00096; NID:G1788623; PIDN:AAC75352.

A:Experimental source: strain K-12, substrain MG1655

Query Match 7.4%; Score 90.5; DB 2; Length 610;

Best Local Similarity 30.8%; Pred. No. 2;

Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

Qy 15 LVLVLL-----GVLNAIPILVSLVEEDFSQN-----PISCFEWMFPGIIGA 58

94 MLVLMILTVAGLGAFMSTGVVAIFIPVLSVANRMQTSPSRLMMPIS-----FAGLI-S 147

Qy 59 GLMAIPATWMSLTARKKACCNRTGMFLSFFS-----VITVIGALYCMILISIQALLKG 112

148 GMMTLVATPPRLVNVNSEL---REGYHGFSFVSVPGLVVLVGLIY--MLVMRFMLKG 202

Db

RESULT 9

A81298

formate dehydrogenase (EC 1.2.1.2) cytochrome B chain Cj1509c [imported] - Campylobacter C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: A81298

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrer Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: A81298

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-310 <PAR>

A:Cross-references: UNIPROT:Q9PMF4; GB:AL139078; GB:AL111168; NID:G6968723; PIDN:CAB7393

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: fdhC; Cj1509c

C:Superfamily: formate dehydrogenase chain C

C:Keywords: oxidoreductase

Query Match 7.4%; Score 89.5; DB 2; Length 310;

Best Local Similarity 18.1%; Pred. No. 1.2;

Matches 49; Conservative 35; Mismatches 64; Indels 123; Gaps 11;

Qy 7 WTCNGFSLVLLTLGV--VLMALPLVSLVEEDFSQNP-----ISCFE 49

48 WTLQGEVIALIALIVAVLSAPALHYMYGPKQFSDGKKIYAFILPERLPIAIS 107

Qy 50 W-----WPGIIGAGLMAIPATWMSLTARKKACCNRTGMFLSFFSVITVIGAL 99

108 WVLIVPTGFWVMFEVVGQGVFV-----RVCKN-----LHAFAIILFIISII 149

Qy 100 YCMILISIQALLKGFLMCSNPSNANCBFSLKNSIDIHPSFNQWPFNDSCAPPTGPNK 159

150 PMFLCWIKRM-----PASVDIRMM----- 170

Qy 160 PTSDWTASGM-----RASFPDSEERKRLIHFSVFLGLLV----- 198

171 -----IVGGLSKIKRPVAKGNFGOKS-----WYIAVVGGLMIITGPFMTFLDPNS 220

Qy 199 GILEVFLGLSQ-----IVIGFLGLCGV 221

221 TAIQGLFGLNQIELLRISAIYVHNFGLIVCAV 251

Db

RESULT 10

T33261
hypothetical protein C2AB9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A:Accession: T33261
R:Murray, J.; Mohlmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid C2AB9.
A:Reference number: Z1310
A:Accession: T33261
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-119 <MUR>
A:Cross-references: UNIPROT:O76434; EMBL:AF068709; PIN:AAIC1249.1; GSPDB:GN00023; CESP:
A:Experimental source: strain Bristol N2; clone C2AB9
C:Genetics:
A:Gene: CESP:C2AB9.6
A:Map position: 5
A:Introns: 19/2; 49/3; 195/3; 239/3
C:Superfamily: Caenorhabditis elegans hypothetical protein t16D9.7

Query Match
Best Local Similarity 7.3%; Score 88.5; DB 2; Length 319;
Matches 42; Conservative 29; Mismatches 50; Indels 93; Gaps 11;

OY 5 EGWTSNCNFSPL-----LVLLILGVVLA--IPLYSLVEEDFQSONPISCFE-WMFPGIIIG 57
| | : || : : : || : : : || : : : || : : : || :
DB 24 EEMSELNGYKRPAGIIIMTYGILMNIVYPIILAVMLEEHFK---MSCFRMTFLGIIV 79
| | : || : : : || : : : || : : : || : : : || :
OY 58 AGLMAIPATYMSLRKKACNNRTGMFLSFFSG-VITTVICALYCM--LISTQALLKGP 113
| | : || : : : || : : : || : : : || : : : || :
DB 80 -----DMALMVNSIIITGFAYQGAVVCYPNLIYISGMAGFG 117
| | : || : : : || : : : || : : : || : : : || :
OY 114 LMCNPSNSNANC-----EFSLKNISDIHPESEF----- 141
| | : || : : : || : : : || : : : || : : : || :
DB 118 LWC-----CSCLTANSVLINRIIDLSKESCKLIPEGAKTYGVLTLPVITYGMVFYIFT 170
| | : || : : : || : : : || : : : || : : : || :
OY 142 -----NLQWFENDSCAP-----PTGFN 158
| | : || : : : || : : : || : : : || : : : || :
DB 171 TPFAFSSKHLTFWFNPULIFPMNTHETVTLPPGFN 204
| | : || : : : || : : : || : : : || : : : || :

RESULT 11

A82357
probable multidrug resistance protein VC0164 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
A:Accession: A82357
R:Heidelberger, U.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Charadon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers,
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:2040683; PMID:10952301
A:Accession: A82357
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1036 <HEI>
A:Cross-references: UNIPROT:O9KV12; GB:AEO04106; GB:AEO03852; NID:g9654561; PIDN:AAF93334
A:Experimental source: serogroup O1, strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0164
A:Map position: 1
C:Superfamily: acriflavine resistance protein

Query Match
Best Local Similarity 7.2%; Score 88; DB 2; Length 1036;
Matches 41; Conservative 18; Mismatches 53; Indels 18; Gaps 7;

12 GFSLVLLILGVVLAIPLYVS-----LVEEDFQSDNPISCFEWMFPGIIGAGLMALPAT 66

Db 380 GFSNNMLTLLAMVL-ALGLVDDDAIVLEANDRHKKESESPPR---AAIIIGREIAIIPYI 435

Qy 67 TMSYLA---RRKRCNNRTGMFLSPFSVITVIGALYCMILSIGALLKGLPMCSPPSS 122

Db 436 AMTLTLGAVPAFIALMGSTIGSLPKEF--ALTLGVSVF--VSGIVALTLSPMWCSKMLKA 491

Qy 123 N-ANCEPSLK 131

Db 492 NEADPKFELK 501

RESULT 12

B82495
Probable NMDH dehydrogenase VCA0157 [imported] - Vibrio cholerae (strain N16961 serogroup O139)
CDate: 18-Aug-2000 #sequence
CDate: 18-Aug-2000 #revision 20-Aug-2000 #text_change 09-Jul-2004

R:Heideberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:2040683; PMID:10952301

A:Accession: B82495

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-891 <HEI>

A:Cross-references: UNIPROT:O9KN09; GB:AE004356; GB:AE003853; NID:G9657536; PIDN:AAF96070

A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:

A:Gene: VCA0157

A:Map position: 2

Query Match 7.1%; Score 86.5; DB 2; Length 891;
Best Local Similarity 22.6%; Pred. No. 6.8;
Matches 30; Conservative 28; Mismatches 34; Indels 41; Gaps 6;

Qy 8 TSCNGFSLLV-LLILGVVLMALPLIVSLVEBDQFSQNPISCFEWWFPGIIGAGLMAIPAT 66

Db 154 TGAGGALLAGIILIGLMANSYQISVIIIEHADHIAQHP-----WFWPSLI---LVLLGAF 205

Qy 67 TMS-----LTARKRACNNRTGMFLSS-----PFSVITVIG 97

Db 206 TKSACPFPHFMLPNMAAPTPVSAYLHSHATWVAGIYLLARLSPIYASSDPFMYCIIIVG 265

Qy 98 ---ALYCMELISIQ 107

Db 266 AVTALMCAIILAKK 278

RESULT 13

AC1340
maltoedextrin ABC-transport system (permease) homolog lmo2123 [imported] - Listeria monocytogenes
CDate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Matrounam, A.; Matok, C.; Schultze, T.; Simoes, N.; Tlterez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.
Article: Comparative genomes of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1340

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-263 <GLA>

A:Cross-references: UNIPROT:O8YSE1; GB:NC_003210; PIDN:CAD00201.1; PID:G16411593; GSPDB:C

C:Genetics:

A:Experimental source: strain EGD-e

A:Gene: lmo2123

C;Superfamily: maltose transport protein malG

Query Match 7.1%; Score 86; DB 2; Length 283;

Best Local Similarity 24.7%; Pred. No. 2.3; Matches 33; Conservative 26; Mismatches 57; Indels 34; Gaps 7;

QY 79 NNETGMFLSSPF-----SVITVIGALYCMILSIQALKGPLMCSNPSNSNA-----NCEP 128

Db 7 DQRTKFLQGFVFLFLVTLITLILVPLILITASARK-----PGNIAFLTEWSDSW 58

QY 129 SLKKNISIHESFNLQWFPNDSCAPPTGKPKPTNSNDTMASGMRASSFHPSEENKRLIH 188

Db 59 TLNNFRLFNFTLIDVYKXVTLIAVVTMTMQVITVLA-GYTSRYRFRGRKNS--LIF 115

QY 189 FSV-----FLGLLVGILEVLPGLSQIVIG 213

Db 116 FLTIQWPTMAALTAFYVLAMLGALDQWFFLIIYIG 153

RESULT 14

H64713 Na+/H+-exchanging protein - Helicobacter pylori (strain 26695)

N;Alternate names: Na+/H+ antiporter

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: H64713

R;Tomb: J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Petereson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: H64713

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-438 <TOM>

A;Cross-references: UNIPROT:Q26076; GB:AE000653; GB:AE000511; NID:g2314733; PIDD:AD0855

C;Superfamily: Na+/H+-exchanging protein nhaa

Query Match 7.1%; Score 86; DB 2; Length 438;

Best Local Similarity 31.5%; Pred. No. 3.6; Matches 34; Conservative 15; Mismatches 39; Indels 20; Gaps 5;

QY 19 LLIGVNTN-----ALPLVSLVEEDQFSQNPISCFEWMFPGITGALMAIPATYMSL- 70

Db 335 VLLGVILGLCLGKPLGIFLTFISEKLTARP-KGISWVH--ILGAGLLAGIGFTWMP 391

QY 71 -----TARRBACCNNRTGMFLSSPFSVITVIGALYCMILSIQALK 111

Db 392 ISNLAFTSEHKDMEVAKIALLGLIS--GIIGALYLPADKRAALK 437

RESULT 15

B82295

prolipoprotein diacylglycerol transferase VC0674 [imported] - Vibrio cholerae (strain NI

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: B82295

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Hardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.

l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: B82295

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-271 <HEI>

A;Cross-references: UNIPROT:O87077; GB:AE004153; GB:AE003852; NID:g9655103; PIDD:AAF9383

C;Genetics:

A;Gene: VC0674

A;Map position: 1
C;Superfamily: prolipoprotein diacylglycerol transferase

Query Match 7.0%; Score 85.5; DB 2; Length 271;

Best Local Similarity 23.1%; Pred. No. 2.4; Matches 53; Conservative 31; Mismatches 100; Indels 45; Gaps 10;

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Db 51 GMTREQVSDLLFAGFLGVIGRAGVYIFYNPDLFLADPLVPRVWVGMSFHGGLGV- 109

QY 65 ATWMSLTARRRACNNRTGMFLSSPFSVITVIG-----ALYCMILSIQALL- 110

Db 110 ITAMFWYARK-----NGRTFFGVADFVAPLVPFGIGMGRIGNFMNSSELMGRVTPVPAVVF 165

QY 111 --KGPLMCSNPSNSNANCEFSLKNISDIHESFNLQWFPNDSCAPPTGPKPTNSNDTMAS 168

Db 166 PNGGFL---PRHPSQLYEFALGVVLF-----FLNMV-----IKPRPLGSGVG 207

QY 169 GMPA--SSPHDSEENKRLIHFSVFLGLLVGILEVLPGLSQIVIGFL 215

Db 208 LPLAGVGTFRFLVYVRPDQAQGLRGFGFSMG---QILSLPMVITIGIL 253

Search completed: January 24, 2005, 15:56:17
Job time : 81 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:42:16 ; Search time 148 Seconds
(without alignments)
559.022 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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626	1215	100.0	229	14	US-10-063-742-48
718	1215	100.0	229	14	US-10-063-550-48
742	1209	99.5	229	13	US-10-087-192-66
743	1205	99.2	229	16	US-10-755-889-508
744	1189	97.9	227	17	US-10-331-053-36
745	924.5	76.1	230	13	US-10-087-192-63
746	907.5	74.7	228	17	US-10-331-053-33
747	173.5	14.3	205	15	US-10-264-049-2362
748	170	14.0	197	11	US-09-973-278-154
749	170	14.0	197	14	US-10-156-136-27
750	170	14.0	198	10	US-09-983-802-232
751	170	14.0	198	10	US-09-984-490-232

752	170	14.0	202	10	US-09-284-320-84	Sequence 84, App1
753	170	14.0	202	14	US-10-060-036-168	Sequence 168, App
754	170	14.0	202	14	US-10-156-136-41	Sequence 41, App1
755	170	14.0	202	14	US-10-334-038-4	Sequence 4, App1
756	170	14.0	202	14	US-10-295-027-1324	Sequence 1324, Ap
757	170	14.0	202	17	US-10-783-528-94	Sequence 94, App1
758	166.5	13.7	202	14	US-10-060-036-4558	Sequence 4558, Ap
759	166.5	13.7	202	14	US-10-295-027-1303	Sequence 1303, Ap
760	166.5	13.7	202	17	US-10-783-528-84	Sequence 84, App1
761	166	13.7	197	14	US-10-156-136-40	Sequence 40, App1
762	144	11.9	153	9	US-09-925-301-1532	Sequence 1532, Ap
763	142	11.6	245	9	US-09-925-297-475	Sequence 475, App
764	140.5	11.7	145	10	US-09-866-050A-723	Sequence 723, App
765	126	10.4	201	14	US-10-156-136-28	Sequence 28, App1
766	126	10.4	201	14	US-10-295-027-10	Sequence 10, App1
767	126	10.4	201	15	US-10-211-462-12	Sequence 12, App1
768	111.5	9.2	209	10	US-09-284-320-7	Sequence 7, App1
769	88	7.2	1036	15	US-10-282-122A-76970	Sequence 76970, A
770	87.5	7.2	117	14	US-10-104-047-3823	Sequence 3823, Ap
771	87	7.2	1174	15	US-10-389-566-742	Sequence 742, App
772	87	7.2	1635	16	US-10-437-963-128533	Sequence 128533, A
773	86.5	7.1	891	15	US-10-282-122A-77590	Sequence 77590, A
774	86	7.1	449	10	US-09-882-227-406	Sequence 406, App
775	85.5	7.0	356	14	US-10-144-929-114	Sequence 114, App
776	85.5	7.0	356	15	US-10-144-929-114	Sequence 114, App
803	85.5	7.0	453	11	US-09-997-428-73	Sequence 73, App1
848	85.5	7.0	453	11	US-09-972-211-119	Sequence 119, App
1312	85.5	7.0	453	14	US-10-174-587-84	Sequence 84, App1
1362	85.5	7.0	453	15	US-10-264-237-2675	Sequence 2675, Ap
1370	85.5	7.0	453	15	US-10-096-625-119	Sequence 119, App
1372	85.5	7.0	453	17	US-10-788-792-182	Sequence 182, App
1373	85.5	7.0	457	11	US-09-972-211-118	Sequence 118, App
1374	85.5	7.0	457	15	US-10-096-625-118	Sequence 118, App
1375	85.5	7.0	472	11	US-09-972-211-120	Sequence 120, App
1376	85.5	7.0	472	14	US-10-153-668-208	Sequence 208, App
1377	85.5	7.0	472	15	US-10-096-625-118	Sequence 120, App
1378	84	6.9	449	15	US-10-335-977-5387	Sequence 5387, Ap
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1381	82.5	6.8	261	11	US-09-833-245-1828	Sequence 1828, Ap
1382	82.5	6.8	1650	16	US-10-437-963-121337	Sequence 121337, A
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1385	82	6.7	867	10	US-09-970-944-37	Sequence 37, App1
1386	82	6.7	867	14	US-10-044-564-134	Sequence 134, App
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1388	81.5	6.7	261	11	US-09-833-245-1827	Sequence 1827, Ap
1389	81.5	6.7	316	10	US-09-795-271-6	Sequence 6, App1
1390	81.5	6.7	1694	14	US-10-203-708-36	Sequence 36, App1
1391	81.5	6.7	1709	14	US-10-203-708-35	Sequence 35, App1
1392	81	6.7	461	14	US-10-369-493-5084	Sequence 5084, Ap
1393	80.5	6.6	430	16	US-10-437-963-127004	Sequence 127004, A
1394	80.5	6.6	930	16	US-10-437-963-113209	Sequence 113209, A
1395	80	6.6	607	16	US-10-437-963-121923	Sequence 121923, A
1396	80	6.6	1056	17	US-10-425-115-184737	Sequence 184737, A
1397	80	6.6	775	16	US-10-437-963-147489	Sequence 147489, A
1398	79	6.5	144	15	US-10-108-260A-2843	Sequence 2843, Ap
1399	79	6.5	212	16	US-10-437-963-158499	Sequence 158499, A
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1404	78	6.4	717	16	US-10-437-963-118126	Sequence 118126, A
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1435	75.5	6.2	681	16	US-10-437-963-160409	Sequence 160409, A
1436	75	6.2	527	15	US-10-282-122A-57071	Sequence 57071, A
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1438	75	6.2	844	16	US-10-437-963-173267	Sequence 173267, A
1439	75	6.2	2108	15	US-10-236-392-184	Sequence 184, App
1440	75	6.2	2167	9	US-09-778-927A-61	Sequence 61, App1
1441	75	6.2	2199	15	US-10-236-392-182	Sequence 182, App
1442	75	6.2	2200	10	US-09-796-575-2	Sequence 2, App11
1443	75	6.2	2200	16	US-10-652-814-2	Sequence 2, App11
1444	75	6.2	2201	13	US-10-100-912-2	Sequence 2, App11
1445	75	6.2	2201	14	US-10-465-572-12	Sequence 12, App1
1446	75	6.2	2201	15	US-10-373-801-34	Sequence 34, App1
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1448	75	6.2	2201	17	US-10-719-993-775	Sequence 775, App
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1474	73.5	6.0	224	17	US-10-425-115-231522	Sequence 231522, A
1475	73.5	6.0	261	10	US-09-940-227-76	Sequence 76, App1

Search completed: January 24, 2005, 15:54:39
Job time : 184 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:42:36 ; Search time 40 Seconds
(without alignments)
379.671 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSILVLL.....IVIGFLGCLGVSKRSQIV 229

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6618000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1500 summaries

Database :

Issued Patents AA: *
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	170	14.0	198	1	US-09-227-357-232
5	170	14.0	202	1	US-08-048-700-2
6	170	14.0	202	2	US-08-855-261A-3
7	170	14.0	202	3	US-08-839-711-3
8	170	14.0	202	3	US-09-227-224-3
9	170	14.0	202	4	US-09-855-288-9
10	160	13.2	202	2	US-08-855-261A-4
11	160	13.2	202	3	US-08-839-711-4
12	160	13.2	202	3	US-09-227-224-4
13	160	13.2	202	4	US-09-855-288-10
14	125	10.3	205	3	US-08-839-711-1
15	85.5	7.0	344	1	US-08-689-974-1
16	85.5	7.0	344	3	US-09-058-376-1
17	81	6.7	254	1	US-08-047-413-9
18	81	6.7	254	3	US-08-229-050-9
19	81	6.7	254	3	US-08-801-563-9
20	79.5	6.5	430	3	US-09-134-001C-2981
21	79.5	6.5	1160	4	US-09-328-352-6826
22	79	6.5	315	4	US-09-134-001C-5446
23	79	6.5	555	4	US-09-543-681A-4582
24	79	6.5	1305	3	US-08-864-785-3
25	79	6.5	1353	3	US-08-894-173-2
26	79	6.5	1353	3	US-09-398-193-2
27	78	6.4	1065	4	US-09-252-991A-31637

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29	77.5	6.4	222	4	US-09-252-991A-26487	Sequence 26487, A
30	76.5	6.3	614	4	US-09-489-039A-12605	Sequence 12605, A
31	76	6.3	337	4	US-09-710-279-444	Sequence 444, App
32	76	6.3	500	4	US-09-543-681A-4601	Sequence 4601, Ap
33	75	6.2	2199	4	US-09-328-352-7936	Sequence 7936, Ap
34	75	6.2	2199	5	US-08-793-273C-2	Sequence 2, Appli
35	75	6.2	2199	5	PCT-US95-11684-2	Sequence 2, Appli
36	75	6.2	2200	4	US-09-796-575-2	Sequence 2, Appli
37	73.5	6.0	624	4	US-09-543-681A-4343	Sequence 4343, Ap
38	73	6.0	203	4	US-09-252-991A-22678	Sequence 22678, A
39	73	6.0	631	3	US-09-345-468-12	Sequence 12, Appli
40	73	6.0	631	3	US-09-414-453A-12	Sequence 12, Appli
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46	72	5.9	475	4	US-09-543-681A-4458	Sequence 4458, Ap
47	72	5.9	741	4	US-09-248-796A-18963	Sequence 18963, A
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52	71.5	5.9	445	4	US-09-710-279-2644	Sequence 2644, Ap
53	71.5	5.9	450	3	US-09-134-001C-4858	Sequence 4858, Ap
54	71	5.8	299	4	US-09-393-634-5	Sequence 5, Appli
55	70.5	5.8	286	3	US-09-333-521-1	Sequence 1, Appli
56	70.5	5.8	319	4	US-09-543-681A-5398	Sequence 5398, Ap
57	70.5	5.8	600	4	US-09-198-452A-397	Sequence 397, App
58	70	5.8	255	4	US-09-302-626B-76	Sequence 76, Appli
59	70	5.8	485	4	US-09-602-787A-614	Sequence 614, App
60	70	5.8	625	4	US-09-489-039A-10099	Sequence 10099, A
61	70	5.8	715	4	US-09-792-024-85	Sequence 85, Appli
62	70	5.8	735	4	US-09-270-767-40232	Sequence 4032, A
63	70	5.8	735	4	US-09-270-767-55448	Sequence 5548, A
64	70	5.8	797	4	US-09-191-468-120	Sequence 120, App
65	70	5.8	797	4	US-09-191-468-122	Sequence 122, App
66	70	5.8	1058	2	US-08-687-289A-5	Sequence 5, Appli
67	70	5.8	1058	4	US-09-435-897-5	Sequence 5, Appli
68	69.5	5.7	172	4	US-09-248-796A-21509	Sequence 21509, A
69	69.5	5.7	235	4	US-09-472-087-14	Sequence 14, Appli
70	69.5	5.7	235	4	US-09-472-087-65	Sequence 65, Appli
71	69.5	5.7	320	4	US-09-543-681A-6667	Sequence 6667, Ap
72	69.5	5.7	347	1	US-08-118-270-47	Sequence 47, Appli
73	69.5	5.7	347	5	PCT-US93-08528-47	Sequence 47, Appli
74	69.5	5.7	1019	4	US-09-252-991A-24417	Sequence 24417, A
75	69	5.7	160	4	US-09-248-796A-24377	Sequence 24377, A
76	69	5.7	245	4	US-09-325-932A-89	Sequence 89, Appli
77	69	5.7	405	2	US-08-700-013B-6	Sequence 6, Appli
78	69	5.7	493	3	US-09-134-001C-3486	Sequence 3486, Ap
79	69	5.7	500	4	US-09-252-991A-25053	Sequence 25053, A
80	69	5.7	797	2	US-08-700-013B-19	Sequence 19, Appli
81	69	5.7	797	3	US-09-182-728A-2	Sequence 2, Appli
82	69	5.7	797	4	US-09-191-468-124	Sequence 124, App
83	69	5.7	797	4	US-09-795-232-2	Sequence 2, Appli
84	69	5.7	2486	3	US-09-125-028-2	Sequence 2, Appli
85	68.5	5.6	208	4	US-09-583-110-1112	Sequence 4112, Ap
86	68.5	5.6	323	4	US-09-619-353-4	Sequence 4, Appli
87	68.5	5.6	356	4	US-09-134-000C-4914	Sequence 4914, Ap
88	68.5	5.6	465	4	US-09-710-279-2928	Sequence 2928, Ap
89	68.5	5.6	467	4	US-09-107-532A-6175	Sequence 6175, Ap
90	68.5	5.6	473	3	US-09-134-001C-3564	Sequence 3564, Ap
91	68.5	5.6	2032	4	US-09-071-035-458	Sequence 458, App
92	68.5	5.6	2032	4	US-09-071-035-462	Sequence 462, App
93	68.5	5.6	2032	4	US-09-071-035-466	Sequence 466, App
94	68.5	5.6	2054	4	US-09-134-000C-6612	Sequence 6612, Ap
95	68	5.6	205	4	US-09-191-468-55	Sequence 55, Appli
96	68	5.6	271	4	US-09-248-796A-14877	Sequence 14877, A
97	68	5.6	320	4	US-09-489-039A-10551	Sequence 10551, A
98	68	5.6	354	2	US-08-700-013B-9	Sequence 9, Appli
99	68	5.6	443	4	US-09-711-164-462	Sequence 462, App
100	68	5.6	443	4	US-09-492-709A-276	Sequence 276, App

101	68	5.6	498	5	PCT-US94-01101-2	Sequence 2, Appl1	174	66	5.4	273	3	US-09-134-001C-3917	Sequence 3917, Ap
102	68	5.6	596	2	US-08-393-806A-2	Sequence 2, Appl1	175	66	5.4	342	4	US-09-054-272-2	Sequence 2, Appl1
103	68	5.6	596	3	US-09-257-490-2	Sequence 2, Appl1	176	66	5.4	345	4	US-09-602-787A-544	Sequence 544, App
104	68	5.6	794	4	US-09-252-991A-22637	Sequence 22637, A	177	66	5.4	352	4	US-09-029-027B-2	Sequence 2, Appl1
105	68	5.6	797	2	US-08-700-013B-21	Sequence 21, Appl	178	66	5.4	376	4	US-09-710-279-490	Sequence 490, App
106	68	5.6	799	2	US-08-700-013B-27	Sequence 27, Appl	179	66	5.4	376	4	US-09-710-279-490	Sequence 2260, Ap
107	68	5.6	1810	4	US-08-793-273C-4	Sequence 4, Appl1	180	66	5.4	482	1	US-07-792-885A-1	Sequence 1, Appl1
108	68	5.6	1810	5	PCT-US95-11684-4	Sequence 4, Appl1	181	66	5.4	482	1	US-08-142-439A-7	Sequence 7, Appl1
109	67.5	5.6	155	4	US-09-107-532A-6942	Sequence 6942, Ap	182	66	5.4	482	2	US-08-869-477-7	Sequence 7, Appl1
110	67.5	5.6	312	4	US-09-393-634-51	Sequence 51, Appl	183	66	5.4	544	4	US-09-107-532A-7350	Sequence 7250, Ap
111	67.5	5.6	317	2	US-08-619-362A-8	Sequence 8, Appl1	184	66	5.4	718	4	US-09-657-960-3	Sequence 7250, Ap
112	67.5	5.6	372	4	US-09-252-991A-26719	Sequence 26719, A	185	66	5.4	877	4	US-09-206-551-20	Sequence 20, Appl
113	67.5	5.6	449	4	US-09-543-681A-6546	Sequence 6546, Ap	186	66	5.4	1353	3	US-09-398-193-99	Sequence 99, Appl
114	67.5	5.6	2161	1	US-07-745-206A-2	Sequence 2, Appl1	187	66	5.4	1451	4	US-09-060-299-25	Sequence 25, Appl
115	67.5	5.6	2161	1	US-08-455-543A-49	Sequence 49, Appl	188	66	5.4	1451	4	US-09-402-923A-25	Sequence 25, Appl
116	67.5	5.6	2161	1	US-08-455-543A-51	Sequence 51, Appl	189	66	5.4	1584	4	US-09-060-299-39	Sequence 39, Appl
117	67.5	5.6	2161	2	US-08-223-305C-49	Sequence 49, Appl	190	66	5.4	1584	4	US-09-402-923A-39	Sequence 39, Appl
118	67.5	5.6	2161	2	US-08-223-305C-51	Sequence 51, Appl	191	66	5.4	1591	4	US-09-060-299-4	Sequence 4, Appl1
119	67.5	5.6	2161	2	US-08-311-363-2	Sequence 2, Appl1	192	66	5.4	1591	4	US-09-060-299-43	Sequence 43, Appl
120	67	5.5	147	4	US-09-134-000C-6018	Sequence 6018, Ap	193	66	5.4	1591	4	US-09-402-923A-4	Sequence 4, Appl1
121	67	5.5	167	4	US-09-191-468-65	Sequence 65, Appl	194	66	5.4	1591	4	US-09-060-299-3	Sequence 43, Appl
122	67	5.5	199	4	US-09-248-796A-14467	Sequence 14467, A	195	66	5.4	1615	4	US-09-060-299-3	Sequence 43, Appl
123	67	5.5	203	4	US-09-270-767-38554	Sequence 38554, A	196	66	5.4	1615	4	US-09-402-923A-3	Sequence 3, Appl1
124	67	5.5	203	4	US-09-270-767-53771	Sequence 53771, A	197	66	5.4	1615	4	US-09-402-923A-3	Sequence 3, Appl1
125	67	5.5	205	4	US-09-191-468-63	Sequence 63, Appl	198	66	5.4	1615	4	US-09-544-398B-3	Sequence 3, Appl1
126	67	5.5	205	4	US-09-191-468-68	Sequence 68, Appl	199	66	5.4	1615	4	US-09-544-398B-4	Sequence 4, Appl1
127	67	5.5	283	4	US-09-134-000C-4870	Sequence 4870, Ap	200	66	5.4	1615	4	US-09-543-771-3	Sequence 3, Appl1
128	67	5.5	287	4	US-09-252-991A-31548	Sequence 31548, A	201	66	5.4	1639	4	US-09-060-299-29	Sequence 29, Appl
129	67	5.5	297	4	US-09-540-236-2296	Sequence 2362, Ap	202	66	5.4	1639	4	US-09-402-923A-29	Sequence 29, Appl
130	67	5.5	339	4	US-09-328-352-4674	Sequence 4674, Ap	203	66	5.4	176	4	US-09-252-991A-25290	Sequence 25290, A
131	67	5.5	342	4	US-09-540-236-2385	Sequence 2385, Ap	204	65.5	5.4	268	3	US-08-965-056-70	Sequence 9, Appl1
132	67	5.5	345	4	US-09-248-796A-26951	Sequence 26951, A	205	65.5	5.4	333	3	US-08-619-362A-9	Sequence 52, Appl
133	67	5.5	376	4	US-09-540-236-3121	Sequence 3121, Ap	206	65.5	5.4	353	3	US-08-838-151A-52	Sequence 55, Appl
134	67	5.5	393	1	US-07-629-1041-3	Sequence 3, Appl1	207	65.5	5.4	398	4	US-09-543-681A-5007	Sequence 5007, Ap
135	67	5.5	448	4	US-09-792-024-101	Sequence 101, App	208	65.5	5.4	536	4	US-09-107-532A-5507	Sequence 5507, Ap
136	67	5.5	486	4	US-09-178-093B-1	Sequence 1, Appl1	209	65.5	5.4	650	1	US-08-121-713D-60	Sequence 60, Appl
137	67	5.5	630	4	US-09-538-092-384	Sequence 384, Appl	210	65.5	5.4	650	1	US-08-835-268-60	Sequence 60, Appl
138	67	5.5	1791	4	US-09-354-147C-42	Sequence 42, Appl	211	65.5	5.4	650	1	US-09-060-692-60	Sequence 60, Appl
139	67	5.5	2958	3	US-08-894-344C-2	Sequence 2, Appl1	212	65.5	5.4	650	2	US-08-833-391-60	Sequence 60, Appl
140	67	5.5	280	4	US-09-270-767-32524	Sequence 32524, A	213	65.5	5.4	650	3	US-09-060-610-60	Sequence 60, Appl
141	66.5	5.5	280	4	US-09-270-767-47741	Sequence 47741, A	214	65.5	5.4	650	3	PCT-US94-10151A-60	Sequence 60, Appl
142	66.5	5.5	353	3	US-08-838-151A-44	Sequence 44, Appl	215	65.5	5.4	1033	4	US-09-252-991A-20611	Sequence 20611, A
143	66.5	5.5	353	3	US-08-838-151A-46	Sequence 46, Appl	216	65.5	5.4	1058	4	US-09-328-352-4276	Sequence 4276, Ap
144	66.5	5.5	376	4	US-09-404-236B-32	Sequence 32, Appl	217	65.5	5.4	1085	3	US-08-484-719B-5	Sequence 5, Appl1
145	66.5	5.5	517	4	US-09-540-236-2403	Sequence 2403, Ap	218	65.5	5.4	1085	1	US-08-484-565-5	Sequence 5, Appl1
146	66.5	5.5	562	4	US-09-328-352-4694	Sequence 4694, Ap	219	65.5	5.4	1085	2	US-08-480-751-5	Sequence 5, Appl1
147	66.5	5.5	585	4	US-09-328-352-6133	Sequence 6133, Ap	220	65.5	5.4	1085	2	US-08-943-986-5	Sequence 5, Appl1
148	66.5	5.5	1027	3	US-09-162-021B-2	Sequence 2, Appl1	221	65.5	5.4	1085	2	US-08-484-719B-5	Sequence 5, Appl1
149	66.5	5.5	1027	4	US-10-268-051-8	Sequence 8, Appl1	222	65.5	5.4	1085	3	US-08-484-719B-5	Sequence 5, Appl1
150	66.5	5.5	1078	1	US-08-485-588-7	Sequence 7, Appl1	223	65.5	5.4	1085	3	US-08-484-719B-5	Sequence 5, Appl1
151	66.5	5.5	1078	1	US-08-484-565-7	Sequence 7, Appl1	224	65.5	5.4	1085	3	US-08-484-719B-5	Sequence 5, Appl1
152	66.5	5.5	1078	2	US-08-480-751-7	Sequence 7, Appl1	225	65.5	5.4	1621	3	US-08-972-927-3	Sequence 3, Appl1
153	66.5	5.5	1078	2	US-08-943-986-7	Sequence 7, Appl1	226	65	5.3	88	4	US-09-621-976-5007	Sequence 5007, Ap
154	66.5	5.5	1078	3	US-08-353-784-7	Sequence 7, Appl1	227	65	5.3	105	4	US-09-489-038A-11705	Sequence 11705, A
155	66.5	5.5	1078	3	US-08-484-719B-7	Sequence 7, Appl1	228	65	5.3	289	4	US-09-489-038A-12627	Sequence 12627, A
156	66.5	5.5	1078	3	US-08-484-558-6	Sequence 6, Appl1	229	65	5.3	367	4	US-09-543-681A-18168	Sequence 18168, Ap
157	66.5	5.5	1088	1	US-08-484-565-6	Sequence 6, Appl1	230	65	5.3	434	4	US-09-328-352-4563	Sequence 4563, Ap
158	66.5	5.5	1088	1	US-08-480-751-6	Sequence 6, Appl1	231	65	5.3	491	4	US-09-543-681A-8251	Sequence 8251, Ap
159	66.5	5.5	1088	2	US-08-943-986-6	Sequence 6, Appl1	232	65	5.3	509	2	US-09-031-392-6	Sequence 6, Appl1
160	66.5	5.5	1088	2	US-08-943-986-6	Sequence 6, Appl1	233	65	5.3	509	3	US-09-299-549-6	Sequence 6, Appl1
161	66.5	5.5	1088	2	US-08-353-784-6	Sequence 6, Appl1	234	65	5.3	509	3	US-09-610-417-6	Sequence 6, Appl1
162	66.5	5.5	1088	3	US-08-484-719B-6	Sequence 6, Appl1	235	65	5.3	580	2	US-08-677-049-12	Sequence 12, Appl
163	66.5	5.5	1088	3	US-08-484-719B-6	Sequence 6, Appl1	236	65	5.3	749	4	US-09-562-737-97	Sequence 97, Appl
164	66.5	5.5	1088	3	US-08-484-159-6	Sequence 6, Appl1	237	65	5.3	863	4	US-09-894-927B-9	Sequence 9, Appl1
165	66.5	5.5	160	4	US-09-270-767-36568	Sequence 36568, A	238	64.5	5.3	186	4	US-09-248-796A-24150	Sequence 24150, Ap
166	66.5	5.4	160	4	US-09-270-767-51785	Sequence 51785, A	239	64.5	5.3	190	4	US-09-543-681A-8168	Sequence 8168, Ap
167	66.5	5.4	205	4	US-09-151-468-57	Sequence 57, Appl	240	64.5	5.3	230	4	US-09-162-476A-4365	Sequence 4365, A
168	66.5	5.4	217	4	US-09-270-767-33957	Sequence 33957, A	241	64.5	5.3	253	1	US-09-610-417-6	Sequence 5, Appl1
169	66.5	5.4	217	4	US-09-270-767-49174	Sequence 49174, A	242	64.5	5.3	258	4	US-09-248-796A-25815	Sequence 25815, A
170	66.5	5.4	236	4	US-09-598-401C-72	Sequence 72, Appl	243	64.5	5.3	282	4	US-09-724-890-16	Sequence 16, Appl
171	66.5	5.4	250	4	US-09-710-627B-1124	Sequence 1124, Ap	244	64.5	5.3	282	4	US-09-724-890-16	Sequence 16, Appl
172	66.5	5.4	255	4	US-09-302-626B-78	Sequence 78, Appl	245	64.5	5.3	282	4	US-09-724-890-16	Sequence 16, Appl
173	66.5	5.4	268	4	US-09-710-279-1830	Sequence 1830, Ap	246	64.5	5.3	317	2	US-08-790-572-3	Sequence 3, Appl1

247	64.5	5.3	317	2	US-09-213-398-3	Sequence 3, Appl1	320	63	5.2	458	3	US-09-292-069A-29	Sequence 29, Appl1
248	64.5	5.3	327	3	US-08-748-506-22	Sequence 22, Appl1	321	63	5.2	458	4	US-09-032-742-10	Sequence 10, Appl1
249	64.5	5.3	337	3	US-08-748-506-22	Sequence 23, Appl1	322	63	5.2	458	4	US-09-767-013-27	Sequence 27, Appl1
250	64.5	5.3	331	4	US-09-830-217-18	Sequence 18, Appl1	323	63	5.2	458	4	US-09-767-013-29	Sequence 29, Appl1
251	64.5	5.3	338	4	US-09-252-991A-27402	Sequence 27402, A	324	63	5.2	458	4	US-09-341-446B-11	Sequence 11, Appl1
252	64.5	5.3	615	2	US-08-663-566A-17	Sequence 17, Appl1	325	63	5.2	458	4	US-09-292-072-27	Sequence 27, Appl1
253	64.5	5.3	615	2	US-08-023-610-17	Sequence 17, Appl1	326	63	5.2	458	4	US-09-292-072-29	Sequence 29, Appl1
254	64.5	5.3	615	2	US-08-288-065A-17	Sequence 17, Appl1	327	63	5.2	458	4	US-09-170-496D-126	Sequence 126, Appl1
255	64.5	5.3	615	2	US-08-362-240A-17	Sequence 17, Appl1	328	63	5.2	458	4	US-09-170-496D-230	Sequence 230, Appl1
256	64.5	5.3	615	5	PCT-US95-10245-17	Sequence 2, Appl1	329	63	5.2	531	4	US-09-248-796A-16160	Sequence 16160, A
257	64.5	5.3	620	1	US-08-301-722A-2	Sequence 2, Appl1	330	63	5.2	532	3	US-09-117-853-2	Sequence 2, Appl1
258	64.5	5.3	718	4	US-09-252-991A-28229	Sequence 28229, A	331	63	5.2	532	4	US-09-911-154-2	Sequence 2, Appl1
259	64.5	5.3	1580	3	US-08-726-320-1	Sequence 1, Appl1	332	63	5.2	532	4	US-09-485-529-2	Sequence 2, Appl1
260	64.5	5.3	1580	3	US-09-208-716-1	Sequence 1, Appl1	333	63	5.2	532	4	US-09-911-514-2	Sequence 2, Appl1
261	64.5	5.3	3177	2	US-08-477-451-4	Sequence 4, Appl1	334	63	5.2	556	4	US-09-538-092-712	Sequence 712, Appl1
262	64	5.3	167	2	US-08-627-610-6	Sequence 6, Appl1	335	63	5.2	571	4	US-09-973-180A-2	Sequence 2, Appl1
263	64	5.3	168	2	US-08-508-735-46	Sequence 46, Appl1	336	63	5.2	571	4	US-09-973-180A-3	Sequence 3, Appl1
264	64	5.3	168	3	US-09-201-139-46	Sequence 46, Appl1	337	63	5.2	571	4	US-09-973-180A-4	Sequence 4, Appl1
265	64	5.3	195	4	US-09-134-000C-5992	Sequence 5992, Ap	338	63	5.2	606	3	US-09-041-236-4	Sequence 4, Appl1
266	64	5.3	205	4	US-09-191-468-61	Sequence 61, Appl1	339	63	5.2	662	4	US-09-771-467C-4	Sequence 4, Appl1
267	64	5.3	332	4	US-09-543-681A-6839	Sequence 6839, Ap	340	63	5.2	682	1	US-07-998-003A-107	Sequence 107, Appl1
268	64	5.3	379	4	US-09-248-796A-22533	Sequence 22533, A	341	63	5.2	682	1	US-08-453-274B-107	Sequence 107, Appl1
269	64	5.3	456	4	US-09-328-352-6174	Sequence 6174, Ap	342	63	5.2	682	1	US-08-453-695A-107	Sequence 107, Appl1
270	64	5.3	484	4	US-09-328-352-7797	Sequence 7797, Ap	343	63	5.2	682	1	US-08-268-161A-107	Sequence 107, Appl1
271	64	5.3	484	4	US-09-489-039A-7690	Sequence 7690, Ap	344	63	5.2	682	2	US-08-453-702A-107	Sequence 107, Appl1
272	64	5.3	579	4	US-09-252-991A-32124	Sequence 32124, A	345	63	5.2	682	3	US-09-099-639-107	Sequence 107, Appl1
273	64	5.3	808	4	US-09-248-796A-17196	Sequence 17196, A	346	63	5.2	682	5	PCT-US93-12588-107	Sequence 107, Appl1
274	64	5.3	1182	3	US-09-293-505-7	Sequence 7, Appl1	347	63	5.2	682	5	PCT-US95-08071-107	Sequence 107, Appl1
275	64	5.3	1182	4	US-09-060-939A-7	Sequence 7, Appl1	348	63	5.2	806	4	US-09-270-767-461A6	Sequence 461A6, A
276	64	5.3	1203	3	US-09-293-505-2	Sequence 2, Appl1	349	63	5.2	806	1	US-07-998-003A-105	Sequence 105, Appl1
277	64	5.3	1203	4	US-09-060-939A-2	Sequence 2, Appl1	350	63	5.2	806	1	US-08-453-695A-105	Sequence 105, Appl1
278	63.5	5.2	178	4	US-09-248-796A-21678	Sequence 21678, A	351	63	5.2	806	1	US-08-453-695A-105	Sequence 105, Appl1
279	63.5	5.2	211	4	US-09-248-796A-20685	Sequence 20685, A	352	63	5.2	806	1	US-08-268-161A-105	Sequence 105, Appl1
280	63.5	5.2	220	4	US-09-602-787A-608	Sequence 608, App	353	63	5.2	806	2	US-08-453-695A-105	Sequence 105, Appl1
281	63.5	5.2	226	4	US-09-315-926A-79	Sequence 79, Appl1	354	63	5.2	806	3	US-09-099-639-105	Sequence 105, Appl1
282	63.5	5.2	240	4	US-09-328-352-7537	Sequence 7537, Ap	355	63	5.2	806	5	PCT-US93-12588-105	Sequence 105, Appl1
283	63.5	5.2	268	3	US-08-965-056-71	Sequence 71, Appl1	356	63	5.2	806	5	PCT-US95-08071-105	Sequence 105, Appl1
284	63.5	5.2	350	4	US-09-252-991A-32358	Sequence 32358, A	357	63	5.2	904	1	US-07-998-003A-97	Sequence 97, Appl1
285	63.5	5.2	398	2	US-08-288-663A-15	Sequence 15, Appl1	358	63	5.2	904	1	US-08-453-274B-97	Sequence 97, Appl1
286	63.5	5.2	400	2	US-08-103-170-9	Sequence 9, Appl1	359	63	5.2	904	1	US-08-453-695A-97	Sequence 97, Appl1
287	63.5	5.2	403	4	US-09-602-787A-606	Sequence 606, App	360	63	5.2	904	1	US-08-268-161A-97	Sequence 97, Appl1
288	63.5	5.2	433	4	US-09-328-352-5746	Sequence 5746, Ap	361	63	5.2	904	2	US-08-453-702A-97	Sequence 97, Appl1
289	63.5	5.2	448	4	US-09-134-000C-3794	Sequence 3794, Ap	362	63	5.2	904	3	US-09-099-639-97	Sequence 97, Appl1
290	63.5	5.2	467	4	US-09-134-000C-6048	Sequence 6048, Ap	363	63	5.2	904	5	PCT-US93-12588-97	Sequence 97, Appl1
291	63.5	5.2	467	4	US-09-540-236-2469	Sequence 2469, Ap	364	63	5.2	904	5	PCT-US95-08071-97	Sequence 97, Appl1
292	63.5	5.2	482	4	US-09-107-532A-6644	Sequence 6644, Ap	365	63	5.2	1233	4	US-09-354-147C-8	Sequence 8, Appl1
293	63.5	5.2	575	4	US-09-248-796A-20353	Sequence 20353, A	366	63	5.2	1234	4	US-09-354-147C-8	Sequence 8, Appl1
294	63.5	5.2	590	4	US-09-248-796A-18826	Sequence 18826, A	367	63	5.2	1234	3	US-09-473-717-2	Sequence 2, Appl1
295	63.5	5.2	597	4	US-09-252-991A-24252	Sequence 24252, A	368	63	5.2	3119	1	US-08-246-982A-16	Sequence 16, Appl1
296	63.5	5.2	1179	4	US-09-792-024-89	Sequence 89, Appl1	369	63	5.2	3119	1	US-08-453-265-16	Sequence 16, Appl1
297	63	5.2	103	4	US-09-248-796A-27772	Sequence 27772, A	370	62.5	5.1	118	4	US-09-248-796A-24261	Sequence 24261, A
298	63	5.2	210	4	US-09-710-279-708	Sequence 708, App	371	62.5	5.1	152	4	US-09-270-767-47052	Sequence 47052, A
299	63	5.2	216	4	US-09-248-796A-14175	Sequence 14175, A	372	62.5	5.1	185	4	US-09-727-769A-6	Sequence 6, Appl1
300	63	5.2	224	3	US-09-134-001C-4608	Sequence 4608, Ap	373	62.5	5.1	186	4	US-09-248-796A-18306	Sequence 18306, A
301	63	5.2	275	4	US-09-489-039A-13172	Sequence 13172, A	374	62.5	5.1	222	4	US-09-270-767-34409	Sequence 34409, A
302	63	5.2	295	2	US-08-679-765-5	Sequence 5, Appl1	375	62.5	5.1	222	4	US-09-270-767-49626	Sequence 49626, A
303	63	5.2	295	2	US-09-196-525-5	Sequence 5, Appl1	376	62.5	5.1	269	2	US-08-484-905-116	Sequence 116, App
304	63	5.2	295	3	US-09-318-317-5	Sequence 5, Appl1	377	62.5	5.1	269	3	US-08-481-985B-116	Sequence 116, App
305	63	5.2	295	4	US-09-177-165A-22	Sequence 22, Appl1	378	62.5	5.1	269	3	US-08-370-478-116	Sequence 478116, A
306	63	5.2	295	4	US-09-538-092-137	Sequence 137, App	379	62.5	5.1	270	4	US-09-270-767-56184	Sequence 56184, A
307	63	5.2	341	4	US-09-248-796A-16208	Sequence 16208, A	380	62.5	5.1	281	4	US-09-270-767-758184	Sequence 758184, A
308	63	5.2	356	4	US-09-134-000C-6394	Sequence 6394, Ap	381	62.5	5.1	282	3	US-09-117-853-8	Sequence 8, Appl1
309	63	5.2	364	4	US-09-252-991A-31716	Sequence 31716, A	382	62.5	5.1	282	4	US-09-911-154-8	Sequence 8, Appl1
310	63	5.2	364	2	US-08-758-621-10	Sequence 10, Appl1	383	62.5	5.1	282	4	US-09-911-154-8	Sequence 8, Appl1
311	63	5.2	376	4	US-09-107-858-10	Sequence 10, Appl1	384	62.5	5.1	315	3	US-08-965-903B-8	Sequence 8, Appl1
312	63	5.2	376	4	US-09-579-174-10	Sequence 10, Appl1	385	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appl1
313	63	5.2	391	4	US-09-107-532A-4615	Sequence 4615, Ap	386	62.5	5.1	315	4	US-09-370-398-6	Sequence 6, Appl1
314	63	5.2	394	4	US-09-252-991A-18502	Sequence 18502, A	387	62.5	5.1	315	4	US-10-090-190-3	Sequence 3, Appl1
315	63	5.2	445	4	US-09-328-352-6669	Sequence 6669, Ap	388	62.5	5.1	315	4	US-10-090-190-6	Sequence 6, Appl1
316	63	5.2	458	1	US-08-310-271-2	Sequence 2, Appl1	389	62.5	5.1	315	4	US-10-082-902-3	Sequence 3, Appl1
317	63	5.2	458	1	US-09-292-071-27	Sequence 27, Appl1	390	62.5	5.1	315	4	US-10-082-902-6	Sequence 6, Appl1
318	63	5.2	458	3	US-09-292-071-29	Sequence 29, Appl1	391	62.5	5.1	319	2	US-08-347-335A-3	Sequence 3, Appl1
319	63	5.2	458	3	US-09-292-069A-27	Sequence 27, Appl1	392	62.5	5.1	320	4	US-09-727-769A-8	Sequence 8, Appl1

393	62.5	5.1	342	3	US-08-785-928-1	Sequence 1, Appl	466	61.5	5.1	249	4	US-09-328-352-6476	Sequence 6476, Ap
394	62.5	5.1	342	3	US-08-728-603-17	Sequence 17, Appl	467	61.5	5.1	267	4	US-09-134-000C-5723	Sequence 5723, Ap
395	62.5	5.1	393	3	US-09-704-725-7	Sequence 7, Appl	468	61.5	5.1	268	4	US-09-248-796A-18304	Sequence 18304, A
396	62.5	5.1	386	3	US-09-086-483A-2	Sequence 2, Appl	469	61.5	5.1	298	4	US-09-134-000C-5845	Sequence 5845, Ap
397	62.5	5.1	386	4	US-09-130-491-6	Sequence 6, Appl	470	61.5	5.1	317	3	US-09-134-001C-5199	Sequence 5199, Ap
398	62.5	5.1	386	4	US-09-580-212-2	Sequence 2, Appl	471	61.5	5.1	326	1	US-08-118-270-39	Sequence 39, Appl
399	62.5	5.1	386	4	US-09-769-402-2	Sequence 2, Appl	472	61.5	5.1	326	5	PCT-US93-08528-39	Sequence 39, Appl
400	62.5	5.1	386	4	US-10-140-002-340	Sequence 340, App	473	61.5	5.1	355	4	US-09-489-039A-9302	Sequence 9302, Ap
401	62.5	5.1	405	4	US-09-543-681A-6109	Sequence 6109, Ap	474	61.5	5.1	370	5	PCT-US93-08528-18	Sequence 18, Appl
402	62.5	5.1	446	4	US-09-328-352-7464	Sequence 7464, Ap	475	61.5	5.1	370	5	PCT-US93-08528-18	Sequence 18, Appl
403	62.5	5.1	478	4	US-09-489-039A-12376	Sequence 12376, A	476	61.5	5.1	488	4	US-09-248-796A-15184	Sequence 15184, A
404	62.5	5.1	485	4	US-09-328-352-8210	Sequence 8210, Ap	477	61.5	5.1	496	4	US-09-489-039A-8772	Sequence 8772, Ap
405	62.5	5.1	486	4	US-09-270-767-42864	Sequence 42864, A	478	61.5	5.1	497	4	US-09-118-693A-1	Sequence 1, Appl
406	62.5	5.1	495	4	US-09-248-796A-22333	Sequence 22333, A	479	61.5	5.1	502	4	US-09-134-000C-6114	Sequence 6114, Ap
407	62.5	5.1	495	4	US-09-252-991A-31450	Sequence 31450, A	480	61.5	5.1	524	1	US-08-529-654-4	Sequence 4, Appl
408	62.5	5.1	556	4	US-09-252-991A-23462	Sequence 23462, A	481	61.5	5.1	542	4	US-09-449-632-4	Sequence 4, Appl
409	62.5	5.1	591	4	US-09-248-796A-14458	Sequence 14458, A	482	61.5	5.1	780	4	US-09-785-381-11	Sequence 11, Appl
410	62.5	5.1	711	4	US-09-134-000C-5325	Sequence 5325, Ap	483	61.5	5.1	866	4	US-09-134-000C-4999	Sequence 4999, Ap
411	62.5	5.1	716	3	US-08-971-188-11	Sequence 11, Appl	484	61.5	5.1	1059	3	US-09-134-513-2	Sequence 2, Appl
412	62.5	5.1	851	4	US-09-543-681A-7277	Sequence 7277, Ap	485	61	5.0	83	4	US-09-621-976-4085	Sequence 4085, Ap
413	62.5	5.1	879	1	US-08-554-612C-1	Sequence 1, Appl	486	61	5.0	108	4	US-09-471-803A-5	Sequence 5, Appl
414	62.5	5.1	1079	1	US-08-485-588-8	Sequence 8, Appl	487	61	5.0	135	4	US-09-270-767-34805	Sequence 34805, A
415	62.5	5.1	1079	1	US-08-484-565-8	Sequence 8, Appl	488	61	5.0	135	4	US-09-270-767-50022	Sequence 50022, A
416	62.5	5.1	1079	2	US-08-480-751-8	Sequence 8, Appl	489	61	5.0	174	3	US-09-383-586-12	Sequence 12, Appl
417	62.5	5.1	1079	2	US-08-943-986-8	Sequence 8, Appl	490	61	5.0	174	4	US-09-383-586-12	Sequence 13, Appl
418	62.5	5.1	1079	3	US-08-353-784-8	Sequence 8, Appl	491	61	5.0	199	3	US-08-737-248-13	Sequence 13, Appl
419	62.5	5.1	1079	3	US-08-484-719B-8	Sequence 8, Appl	492	61	5.0	203	4	US-09-248-796A-16898	Sequence 16898, A
420	62.5	5.1	1079	3	US-08-484-159-8	Sequence 8, Appl	493	61	5.0	213	3	US-08-807-300-4	Sequence 4, Appl
421	62.5	5.1	1881	3	US-09-223-086-3	Sequence 3, Appl	494	61	5.0	219	4	US-08-311-731A-305	Sequence 305, App
422	62	5.1	113	4	US-09-328-352-7133	Sequence 7133, Ap	495	61	5.0	220	4	US-09-205-258-1129	Sequence 1129, Ap
423	62	5.1	137	4	US-09-252-991A-29023	Sequence 29023, A	496	61	5.0	221	4	US-09-248-796A-15458	Sequence 15458, A
424	62	5.1	150	3	US-08-862-124-5	Sequence 5, Appl	497	61	5.0	224	4	US-09-472-087-17	Sequence 17, Appl
425	62	5.1	185	4	US-09-324-910-6	Sequence 6, Appl	498	61	5.0	234	4	US-09-107-532A-4920	Sequence 69, Appl
426	62	5.1	185	4	US-09-793-495-6	Sequence 6, Appl	499	61	5.0	255	4	US-09-270-767-37980	Sequence 4920, Ap
427	62	5.1	216	4	US-09-294-298A-7	Sequence 7, Appl	500	61	5.0	286	4	US-09-270-767-53197	Sequence 37980, A
428	62	5.1	230	4	US-09-663-600A-186	Sequence 186, App	501	61	5.0	287	4	US-09-489-039A-8466	Sequence 8466, Ap
429	62	5.1	230	4	US-10-140-002-492	Sequence 492, App	502	61	5.0	297	4	US-09-489-039A-8466	Sequence 8466, Ap
430	62	5.1	261	4	US-09-248-796A-18760	Sequence 18760, A	503	61	5.0	300	4	US-09-252-991A-17878	Sequence 17878, A
431	62	5.1	266	4	US-09-540-236-2374	Sequence 2374, Ap	504	61	5.0	330	4	US-09-134-000C-3733	Sequence 3733, Ap
432	62	5.1	287	2	US-08-433-783-37	Sequence 37, Appl	505	61	5.0	308	4	US-09-252-991A-23958	Sequence 23958, A
433	62	5.1	287	2	US-08-337-358-37	Sequence 37, Appl	506	61	5.0	325	4	US-09-461-325-141	Sequence 141, App
434	62	5.1	287	5	PCT-US95-07537A-37	Sequence 37, Appl	507	61	5.0	325	4	US-10-012-542-141	Sequence 141, App
435	62	5.1	287	5	PCT-US95-07537-37	Sequence 37, Appl	508	61	5.0	335	4	US-10-115-123-141	Sequence 141, App
436	62	5.1	290	4	US-09-252-991A-18337	Sequence 18337, A	509	61	5.0	335	4	US-09-801-874-5	Sequence 5, Appl
437	62	5.1	294	1	US-08-628-291-2	Sequence 2, Appl	510	61	5.0	391	4	US-09-107-532A-4209	Sequence 4209, Ap
438	62	5.1	294	2	US-09-128-722-2	Sequence 2, Appl	511	61	5.0	426	4	US-09-491-577-46	Sequence 46, Appl
439	62	5.1	294	4	US-09-326-157-1	Sequence 1, Appl	512	61	5.0	435	4	US-09-252-991A-17254	Sequence 17254, A
440	62	5.1	294	4	US-10-135-755-1	Sequence 1, Appl	513	61	5.0	441	4	US-09-252-991A-32306	Sequence 32306, A
441	62	5.1	302	4	US-09-270-767-40028	Sequence 40028, A	514	61	5.0	446	4	US-09-543-681A-6579	Sequence 6579, Ap
442	62	5.1	302	1	US-09-270-767-55244	Sequence 55244, A	515	61	5.0	453	4	US-09-489-039A-8916	Sequence 8916, Ap
443	62	5.1	318	1	US-08-628-291-16	Sequence 16, Appl	516	61	5.0	460	4	US-09-543-681A-8195	Sequence 8195, Ap
444	62	5.1	318	2	US-09-128-722-16	Sequence 16, Appl	517	61	5.0	494	3	US-09-126-420A-26	Sequence 26, Appl
445	62	5.1	319	3	US-09-324-910-12	Sequence 12, Appl	518	61	5.0	506	4	US-09-543-681A-8246	Sequence 8246, Ap
446	62	5.1	319	4	US-09-793-495-12	Sequence 12, Appl	519	61	5.0	518	4	US-09-248-796A-20772	Sequence 20772, A
447	62	5.1	341	4	US-09-248-796A-20844	Sequence 20844, A	520	61	5.0	529	3	US-09-500-063-2	Sequence 2, Appl
448	62	5.1	377	4	US-09-248-796A-15498	Sequence 15498, A	521	61	5.0	568	4	US-09-543-681A-5558	Sequence 5558, Ap
449	62	5.1	399	4	US-09-489-039A-8272	Sequence 8272, Ap	522	61	5.0	574	3	US-09-383-586-36	Sequence 36, Appl
450	62	5.1	409	4	US-09-248-796A-14863	Sequence 14863, A	523	61	5.0	574	4	US-09-823-038A-36	Sequence 36, Appl
451	62	5.1	448	4	US-09-583-110-4040	Sequence 4040, Ap	524	61	5.0	655	4	US-09-252-991A-17469	Sequence 17469, A
452	62	5.1	516	4	US-09-489-039A-12893	Sequence 12893, A	525	61	5.0	865	4	US-09-720-317A-31	Sequence 31, Appl
453	62	5.1	516	3	US-09-310-463-50	Sequence 20, Appl	526	61	5.0	852	4	US-09-206-551-19	Sequence 19, Appl
454	62	5.1	631	4	US-08-842-248A-21	Sequence 21, Appl	527	61	5.0	1279	4	US-09-170-4960-283	Sequence 283, App
455	62	5.1	1135	4	US-09-294-298A-20	Sequence 20, Appl	528	61	5.0	1279	4	US-09-164-425B-58	Sequence 58, Appl
456	62	5.1	1325	4	US-09-294-298A-6	Sequence 6, Appl	529	61	5.0	1765	4	US-09-354-147C-5	Sequence 5, Appl
457	62	5.1	1376	4	US-09-294-298A-4	Sequence 4, Appl	530	61	5.0	3169	2	US-08-477-451-6	Sequence 6, Appl
458	62	5.1	1423	4	US-09-294-298A-2	Sequence 2, Appl	531	60.5	5.0	102	4	US-09-270-767-58664	Sequence 58664, A
459	62	5.1	1423	2	US-08-457-273B-8	Sequence 8, Appl	532	60.5	5.0	117	4	US-08-311-731A-342	Sequence 342, App
460	61.5	5.1	78	4	US-09-543-681A-5110	Sequence 5110, Ap	533	60.5	5.0	182	4	US-09-248-796A-25278	Sequence 25278, A
461	61.5	5.1	86	4	US-09-270-767-58811	Sequence 58811, A	534	60.5	5.0	182	4	US-09-621-976-4128	Sequence 4128, Ap
462	61.5	5.1	148	4	US-09-270-767-45975	Sequence 45975, A	535	60.5	5.0	202	4	US-09-248-796A-19348	Sequence 19348, A
463	61.5	5.1	182	4	US-09-710-279-1354	Sequence 1354, Ap	536	60.5	5.0	269	3	US-08-965-056-42	Sequence 42, Appl
464	61.5	5.1	186	3	US-09-134-001C-4741	Sequence 4741, Ap	537	60.5	5.0	277	4	US-09-583-110-2944	Sequence 2944, Ap
465	61.5	5.1	205	6	5482709-4	Patent No. 5482709	538	60.5	5.0	369	4	US-09-252-991A-18429	Sequence 18429, A

539	60.5	5.0	381	4	US-09-248-796A-19481	Sequence 19481, A	612	59.5	4.9	243	3	US-08-965-056-73	Sequence 73, Appl
540	60.5	5.0	390	4	US-09-198-452A-254	Sequence 254, App	613	59.5	4.9	279	4	US-09-248-796A-25140	Sequence 25140, A
541	60.5	5.0	424	4	US-09-252-991A-18895	Sequence 18895, A	614	59.5	4.9	329	4	US-09-198-452A-363	Sequence 363, App
542	60.5	5.0	448	4	US-09-361-443-4	Sequence 4, Appli	615	59.5	4.9	337	3	US-08-448-722A-2	Sequence 2, Appli
543	60.5	5.0	467	4	US-09-361-443-2	Sequence 2, Appli	616	59.5	4.9	337	3	US-08-189-309B-2	Sequence 2, Appli
544	60.5	5.0	469	4	US-09-198-452A-793	Sequence 793, App	617	59.5	4.9	373	4	US-09-134-000C-4099	Sequence 4099, Ap
545	60.5	5.0	533	4	US-09-107-532A-5244	Sequence 5244, Ap	618	59.5	4.9	406	4	US-09-489-039A-8267	Sequence 8267, Ap
546	60.5	5.0	681	3	US-09-760-615-4	Sequence 4, Appli	619	59.5	4.9	419	4	US-09-489-039A-12928	Sequence 12928, A
547	60.5	5.0	681	3	US-09-336-910A-2	Sequence 2, Appli	620	59.5	4.9	427	4	US-09-252-991A-31904	Sequence 31904, A
548	60.5	5.0	805	3	US-08-989-299-2	Sequence 2, Appli	621	59.5	4.9	470	4	US-09-543-681A-4625	Sequence 4625, Ap
549	60.5	5.0	805	4	US-10-158-847-142	Sequence 142, App	622	59.5	4.9	477	4	US-09-134-000C-6123	Sequence 6123, Ap
550	60.5	5.0	805	4	US-09-407-427-2	Sequence 2, Appli	623	59.5	4.9	480	2	US-08-724-394A-11	Sequence 11, Appli
551	60.5	5.0	905	1	US-08-072-574-2	Sequence 2, Appli	624	59.5	4.9	483	2	US-08-307-485A-1	Sequence 1, Appli
552	60	4.9	87	4	US-09-252-991A-30361	Sequence 30361, A	625	59.5	4.9	483	2	US-08-465-009-2	Sequence 2, Appli
553	60	4.9	87	4	US-09-107-532A-6457	Sequence 6457, Ap	626	59.5	4.9	483	3	US-08-477-928A-2	Sequence 40, Appl
554	60	4.9	125	4	US-09-198-452A-1172	Sequence 1172, Ap	627	59.5	4.9	483	3	US-08-477-928A-40	Sequence 43300, A
555	60	4.9	141	4	US-09-198-452A-1173	Sequence 1173, Ap	628	59.5	4.9	555	4	US-09-270-767-73300	Sequence 4802, Ap
556	60	4.9	158	4	US-09-270-767-8728	Sequence 38728, A	629	59.5	4.9	562	4	US-09-328-352-4802	Sequence 23, Appl
557	60	4.9	158	4	US-09-270-767-53945	Sequence 53945, A	630	59.5	4.9	563	4	US-09-535-315-23	Sequence 30, Appl
558	60	4.9	205	4	US-09-191-468-59	Sequence 59, Appl	631	59.5	4.9	577	1	US-07-820-154A-30	Sequence 23, Appl
559	60	4.9	211	4	US-09-130-491-4	Sequence 4, Appli	632	59.5	4.9	577	2	US-08-663-566A-11	Sequence 10, Appl
560	60	4.9	211	4	US-09-603-552-12	Sequence 12, Appl	633	59.5	4.9	577	2	US-08-097-554A-30	Sequence 11, Appl
561	60	4.9	211	4	US-09-886-683A-4	Sequence 4, Appli	634	59.5	4.9	577	2	US-08-023-610-11	Sequence 11, Appl
562	60	4.9	214	4	US-09-489-039A-12637	Sequence 12637, A	635	59.5	4.9	577	2	US-08-288-065A-11	Sequence 11, Appl
563	60	4.9	218	4	US-09-252-991A-22136	Sequence 22136, A	636	59.5	4.9	577	2	US-08-362-240A-11	Sequence 11, Appl
564	60	4.9	227	2	US-08-254-493-1	Sequence 1, Appli	637	59.5	4.9	577	3	US-08-480-640A-30	Sequence 30, Appl
565	60	4.9	227	2	US-08-253-751-6	Sequence 6, Appli	638	59.5	4.9	577	3	US-08-295-802-30	Sequence 30, Appl
566	60	4.9	227	2	US-08-453-925-6	Sequence 6, Appli	639	59.5	4.9	577	3	US-08-804-372A-9	Sequence 9, Appli
567	60	4.9	227	2	US-08-403-253A-6	Sequence 6, Appli	640	59.5	4.9	577	3	US-08-488-237A-30	Sequence 30, Appl
568	60	4.9	227	4	US-08-435-816A-6	Sequence 6, Appli	641	59.5	4.9	577	3	US-08-375-992A-30	Sequence 30, Appl
569	60	4.9	228	1	US-08-408-222B-1	Sequence 1, Appli	642	59.5	4.9	577	4	US-08-472-679H-30	Sequence 30, Appl
570	60	4.9	233	2	US-09-024-848-4	Sequence 4, Appli	643	59.5	4.9	577	5	PCT-US93-00324-30	Sequence 30, Appl
571	60	4.9	233	3	US-09-348-116A-4	Sequence 4, Appli	644	59.5	4.9	577	5	PCT-US95-10245-11	Sequence 11, Appl
572	60	4.9	239	4	US-09-270-767-44514	Sequence 44514, A	645	59.5	4.9	581	2	US-08-484-575A-13	Sequence 13, Appl
573	60	4.9	259	4	US-09-270-767-38568	Sequence 38568, A	646	59.5	4.9	581	3	US-08-477-459-13	Sequence 13, Appl
574	60	4.9	259	4	US-09-270-767-53785	Sequence 53785, A	647	59.5	4.9	581	3	US-08-479-869-13	Sequence 13, Appl
575	60	4.9	275	4	US-09-270-767-48250	Sequence 48250, A	648	59.5	4.9	581	3	US-08-486-414-13	Sequence 13, Appl
576	60	4.9	329	4	US-09-604-957-2	Sequence 2, Appli	649	59.5	4.9	581	5	PCT-US94-01826A-13	Sequence 13, Appl
577	60	4.9	365	3	US-08-155-005A-8	Sequence 8, Appli	650	59.5	4.9	581	5	PCT-US94-02252A-13	Sequence 13, Appl
578	60	4.9	365	3	US-09-363-783-8	Sequence 8, Appli	651	59.5	4.9	586	4	US-09-583-110-3470	Sequence 3470, Ap
579	60	4.9	365	4	US-09-661-758A-8	Sequence 8, Appli	652	59.5	4.9	621	4	US-09-720-317A-26	Sequence 26, Appl
580	60	4.9	388	3	US-08-155-005A-6	Sequence 6, Appli	653	59.5	4.9	646	4	US-09-720-317A-26	Sequence 26, Appl
581	60	4.9	388	3	US-09-363-783-6	Sequence 6, Appli	654	59.5	4.9	658	4	US-09-720-317A-24	Sequence 24, Appl
582	60	4.9	388	4	US-09-661-758A-6	Sequence 6, Appli	655	59.5	4.9	711	4	US-10-158-847-138	Sequence 138, App
583	60	4.9	390	3	US-08-155-005A-4	Sequence 4, Appli	656	59.5	4.9	717	4	US-09-583-110-4629	Sequence 4629, Ap
584	60	4.9	390	3	US-08-155-005A-17	Sequence 17, Appl	657	59.5	4.9	746	4	US-09-548-797B-4	Sequence 4, Appli
585	60	4.9	390	3	US-09-363-783-4	Sequence 4, Appli	658	59.5	4.9	920	4	US-09-489-039A-12856	Sequence 12856, A
586	60	4.9	390	3	US-09-363-783-17	Sequence 17, Appl	659	59.5	4.9	1053	4	US-09-538-092-1197	Sequence 1197, Ap
587	60	4.9	390	4	US-09-661-758A-4	Sequence 4, Appli	660	59.5	4.9	1053	4	US-09-328-352-5058	Sequence 5058, Ap
588	60	4.9	390	4	US-09-661-758A-17	Sequence 17, Appl	661	59.5	4.9	1081	3	US-09-369-364A-17	Sequence 17, Appl
589	60	4.9	405	3	US-09-134-001C-4999	Sequence 4999, Ap	662	59.5	4.9	1237	1	US-08-241-853-2	Sequence 2, Appli
590	60	4.9	455	4	US-09-489-039A-12823	Sequence 12823, A	663	59.5	4.9	1237	2	US-08-850-917-2	Sequence 2, Appli
591	60	4.9	462	4	US-09-710-279-906	Sequence 906, App	664	59.5	4.9	1289	1	US-08-542-003-2	Sequence 2, Appli
592	60	4.9	491	3	US-09-134-001C-4612	Sequence 4612, Ap	665	59.5	4.9	1289	2	US-08-332-760A-2	Sequence 2, Appli
593	60	4.9	571	4	US-09-328-352-4633	Sequence 4633, Ap	666	59.5	4.9	1289	4	US-09-236-949-2	Sequence 27, Appli
594	60	4.9	633	4	US-09-248-796A-20407	Sequence 20407, A	667	59.5	4.9	1584	3	US-09-457-0408-27	Sequence 27, Appli
595	60	4.9	744	4	US-09-252-991A-30945	Sequence 30945, A	668	59	4.9	155	2	US-08-801-872-1	Sequence 1, Appli
596	60	4.9	838	4	US-09-894-998A-45	Sequence 45, Appl	669	59	4.9	155	3	US-09-178-881-1	Sequence 1, Appli
597	60	4.9	934	4	US-09-252-991A-19515	Sequence 19515, A	670	59	4.9	225	4	US-09-107-532A-4090	Sequence 4090, Ap
598	60	4.9	1059	4	US-09-489-039A-10044	Sequence 10044, A	671	59	4.9	230	4	US-09-663-600A-92	Sequence 92, Appl
599	60	4.9	1543	4	US-09-904-987-7	Sequence 7, Appli	672	59	4.9	278	4	US-09-270-767-59700	Sequence 59700, A
600	60	4.9	2476	2	US-08-276-967-2	Sequence 2, Appli	673	59	4.9	292	2	US-09-024-848-2	Sequence 2, Appli
601	60	4.9	3144	1	US-08-246-982A-6	Sequence 6, Appli	674	59	4.9	292	3	US-09-348-116A-2	Sequence 2, Appli
602	60	4.9	3144	1	US-08-453-265-6	Sequence 6, Appli	675	59	4.9	292	4	US-09-583-110-4530	Sequence 4530, Ap
603	60	4.9	3144	2	US-08-457-273B-42	Sequence 42, Appl	676	59	4.9	293	4	US-09-252-991A-33017	Sequence 33017, A
604	60	4.9	3144	3	US-08-556-419-21	Sequence 21, Appl	677	59	4.9	300	4	US-09-252-991A-26038	Sequence 26038, A
605	60	4.9	3144	3	US-09-041-886-15	Sequence 15, Appl	678	59	4.9	304	4	US-09-134-000C-5201	Sequence 5201, Ap
606	60	4.9	3144	4	US-09-538-092-1118	Sequence 1118, Ap	679	59	4.9	310	4	US-09-907-794A-423	Sequence 423, App
607	60	4.9	1444	4	US-09-107-532A-4029	Sequence 4029, App	680	59	4.9	310	4	US-09-905-125A-423	Sequence 423, App
608	59.5	4.9	169	4	US-09-489-039A-8944	Sequence 8944, Ap	681	59	4.9	310	4	US-09-902-775A-423	Sequence 423, App
609	59.5	4.9	178	4	US-09-446-959-10	Sequence 10, Appl	682	59	4.9	310	4	US-09-906-700-423	Sequence 423, App
610	59.5	4.9	189	4	US-09-134-000C-5408	Sequence 5408, Ap	683	59	4.9	310	4	US-10-140-002-538	Sequence 538, App
611	59.5	4.9	208	4	US-10-140-002-510	Sequence 510, App	684	59	4.9	310	4	US-09-903-603A-423	Sequence 423, App

685	59	4.9	318	4	US-09-540-236-2086	Sequence 2086, Ap	758	58.5	4.8	226	2	US-08-889-666-26	Sequence 26, Appl
686	59	4.9	339	4	US-09-252-991A-19350	Sequence 19350, A	759	58.5	4.8	226	2	US-08-465-078-26	Sequence 26, Appl
687	59	4.9	342	3	US-09-134-001C-4190	Sequence 4190, Ap	760	58.5	4.8	226	2	US-08-725-776-26	Sequence 26, Appl
688	59	4.9	368	1	US-07-977-630-4	Sequence 4, Appli	761	58.5	4.8	226	2	US-08-488-062-26	Sequence 26, Appl
689	59	4.9	368	4	US-09-252-991A-29907	Sequence 29907, A	762	58.5	4.8	223	4	US-09-472-087-15	Sequence 15, Appl
690	59	4.9	374	2	US-08-820-170A-25	Sequence 25, Appl	763	58.5	4.8	223	4	US-09-472-087-67	Sequence 67, Appl
691	59	4.9	374	3	US-09-055-699-35	Sequence 25, Appl	764	58.5	4.8	224	4	US-09-252-991A-22915	Sequence 22915, A
692	59	4.9	374	3	US-09-273-565-35	Sequence 25, Appl	765	58.5	4.8	228	4	US-09-270-767-41633	Sequence 14633, A
693	59	4.9	374	3	US-09-565-538-35	Sequence 25, Appl	766	58.5	4.8	222	4	US-09-489-039A-13487	Sequence 13487
694	59	4.9	374	3	US-09-661-468-35	Sequence 25, Appl	767	58.5	4.8	232	4	US-09-522-714-20	Sequence 20, Appl
695	59	4.9	374	4	US-09-976-165-35	Sequence 25, Appl	768	58.5	4.8	233	3	US-07-791-931-9	Sequence 9, Appli
696	59	4.9	374	4	US-09-227-853A-2	Sequence 2, Appli	769	58.5	4.8	233	4	US-09-270-767-43668	Sequence 43668, A
697	59	4.9	374	5	PCT-US95-06385-2	Sequence 2, Appli	770	58.5	4.8	268	3	US-08-965-056-10	Sequence 10, Appl
698	59	4.9	405	4	US-09-270-767-45879	Sequence 45879, A	771	58.5	4.8	275	4	US-09-252-991A-27808	Sequence 27808, A
699	59	4.9	410	4	US-09-270-767-44276	Sequence 44276, A	772	58.5	4.8	281	4	US-09-489-039A-8675	Sequence 8675, Ap
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701	59	4.9	417	4	US-09-252-991A-25870	Sequence 25870, A	774	58.5	4.8	284	4	US-09-710-279-1688	Sequence 1688, Ap
702	59	4.9	430	4	US-09-134-000C-4819	Sequence 4819, Ap	775	58.5	4.8	229	4	US-09-393-634-41	Sequence 41, Appl
703	59	4.9	444	4	US-09-721-870-42	Sequence 42, Appl	776	58.5	4.8	306	4	US-09-252-991A-22836	Sequence 22836, A
704	59	4.9	467	4	US-09-252-991A-18633	Sequence 18633, A	777	58.5	4.8	338	4	US-09-248-796A-22866	Sequence 22866, A
705	59	4.9	471	4	US-09-711-164-444	Sequence 444, App	778	58.5	4.8	339	2	US-08-758-621-2	Sequence 2, Appli
706	59	4.9	471	4	US-09-492-709A-284	Sequence 284, App	779	58.5	4.8	339	3	US-09-107-858-2	Sequence 2, Appli
707	59	4.9	476	4	US-09-529-157-4	Sequence 4, Appli	780	58.5	4.8	339	4	US-09-579-174-2	Sequence 2, Appli
708	59	4.9	505	4	US-09-328-352-4724	Sequence 4724, Ap	781	58.5	4.8	348	1	US-08-454-196-8	Sequence 8, Appli
709	59	4.9	545	4	US-10-067-422-11	Sequence 11, Appl	782	58.5	4.8	348	1	US-08-454-196-17	Sequence 17, Appl
710	59	4.9	545	4	US-08-272-285-8	Sequence 8, Appli	783	58.5	4.8	348	3	US-09-064-033-8	Sequence 8, Appli
711	59	4.9	566	2	PCT-US95-08565-8	Sequence 8, Appli	784	58.5	4.8	348	3	US-09-064-033-17	Sequence 17, Appl
712	59	4.9	570	4	US-09-489-039A-9421	Sequence 9421, Ap	785	58.5	4.8	348	4	US-09-291-046-8	Sequence 8, Appli
713	59	4.9	572	4	US-09-197-970B-5	Sequence 5, Appli	786	58.5	4.8	348	4	US-09-291-046-17	Sequence 17, Appl
714	59	4.9	577	4	US-09-514-245-3	Sequence 5, Appli	787	58.5	4.8	348	4	US-09-270-767-58705	Sequence 58705, A
715	59	4.9	639	4	US-09-538-092-17	Sequence 17, Appl	788	58.5	4.8	360	4	US-09-489-039A-6049	Sequence 6049, Ap
716	59	4.9	641	4	US-09-252-991A-26994	Sequence 26994, A	789	58.5	4.8	336	4	US-09-549-110-4102	Sequence 13352, A
717	59	4.9	666	4	US-09-489-039A-12388	Sequence 12388, A	790	58.5	4.8	332	4	US-09-248-796A-26952	A Sequence 26952, A
718	59	4.9	694	3	US-09-440-325A-1	Sequence 1, Appli	791	58.5	4.8	336	4	US-09-248-796A-20434	Sequence 20434, A
719	59	4.9	694	4	US-09-846-986A-1	Sequence 1, Appli	792	58.5	4.8	327	4	US-09-370-767-43356	Sequence 43356, A
720	59	4.9	855	4	US-09-107-532A-5646	Sequence 5646, Ap	793	58.5	4.8	420	4	US-09-198-452A-533	Sequence 533, App
721	59	4.9	1203	3	US-09-207-857-2	Sequence 2, Appli	794	58.5	4.8	425	4	US-09-134-000C-5971	Sequence 5971, Ap
722	59	4.9	1203	4	US-09-909-280A-2	Sequence 2, Appli	795	58.5	4.8	426	4	US-09-583-110-4102	Sequence 4102, Ap
723	59	4.9	1296	4	US-08-857-636-80	Sequence 60, Appl	796	58.5	4.8	431	4	US-09-583-110-4734	Sequence 4734, Ap
724	59	4.9	1692	3	US-09-263-933-4	Sequence 4, Appli	797	58.5	4.8	447	4	US-09-489-039A-11893	Sequence 11893, A
725	59	4.9	1692	3	US-09-263-933-11	Sequence 11, Appl	798	58.5	4.8	453	4	US-09-800-729-83	Sequence 83, Appl
726	59	4.9	1692	3	US-09-263-933-18	Sequence 18, Appl	799	58.5	4.8	469	4	US-09-489-039A-10214	Sequence 10214, A
727	59	4.9	1692	3	US-09-919-901-4	Sequence 4, Appli	800	58.5	4.8	466	4	US-08-622-191-7	Sequence 7, Appli
728	59	4.9	1692	4	US-09-919-901-11	Sequence 11, Appl	801	58.5	4.8	488	4	US-10-162-012-46	Sequence 46, Appl
729	59	4.9	1692	4	US-09-919-901-18	Sequence 18, Appl	802	58.5	4.8	511	4	US-09-107-532A-6112	Sequence 6112, Ap
730	59	4.9	1692	4	US-10-191-966-4	Sequence 4, Appli	803	58.5	4.8	545	4	US-09-572-147-2	Sequence 2, Appli
731	59	4.9	1692	4	US-10-191-966-11	Sequence 11, Appl	804	58.5	4.8	550	4	US-09-330-245A-2	Sequence 2, Appli
732	59	4.9	1692	4	US-10-191-966-18	Sequence 18, Appl	805	58.5	4.8	550	4	US-09-614-691-7	Sequence 7, Appli
733	59	4.9	2307	3	US-09-263-933-2	Sequence 2, Appli	806	58.5	4.8	554	3	US-08-943-714-2	Sequence 2, Appli
734	59	4.9	2307	3	US-09-263-933-9	Sequence 9, Appli	807	58.5	4.8	578	4	US-09-248-796A-19477	Sequence 19477, A
735	59	4.9	2307	3	US-09-263-933-16	Sequence 16, Appl	808	58.5	4.8	555	3	US-08-842-079-18	Sequence 18, Appl
736	59	4.9	2307	4	US-09-919-901-2	Sequence 2, Appli	809	58.5	4.8	595	3	US-08-842-079-20	Sequence 20, Appl
737	59	4.9	2307	4	US-09-919-901-9	Sequence 9, Appli	810	58.5	4.8	595	4	US-09-638-857-18	Sequence 18, Appl
738	59	4.9	2307	4	US-09-919-901-16	Sequence 16, Appl	811	58.5	4.8	595	4	US-09-638-857-20	Sequence 20, Appl
739	59	4.9	2307	4	US-10-191-966-2	Sequence 2, Appli	812	58.5	4.8	627	4	US-09-538-092-760	Sequence 760, App
740	59	4.9	2307	4	US-10-191-966-9	Sequence 9, Appli	813	58.5	4.8	635	2	US-09-014-969-11	Sequence 11, Appl
741	59	4.9	2307	4	US-10-191-966-16	Sequence 16, Appl	814	58.5	4.8	660	4	US-09-720-317A-30	Sequence 30, Appl
742	59	4.9	2307	4	US-09-919-497-70	Sequence 70, Appl	815	58.5	4.8	666	3	US-09-341-587-1	Sequence 1, Appli
743	59	4.9	108	4	US-09-270-767-37995	Sequence 37995, A	816	58.5	4.8	668	4	US-09-252-991A-22341	Sequence 22341, A
744	59	4.9	108	4	US-09-270-767-53122	Sequence 53122, A	817	58.5	4.8	661	4	US-09-248-796A-20857	Sequence 20857, A
745	58.5	4.8	129	2	US-08-480-774A-4	Sequence 4, Appli	818	58.5	4.8	691	4	US-09-575-081B-2	Sequence 2, Appli
746	58.5	4.8	130	4	US-09-248-796A-18320	Sequence 18320, A	819	58.5	4.8	903	4	US-09-252-991A-17937	Sequence 17937, A
747	58.5	4.8	136	4	US-09-513-999C-6373	Sequence 6373, Ap	820	58.5	4.8	907	4	US-09-170-496D-264	Sequence 264, App
748	58.5	4.8	142	4	US-09-380-882-9	Sequence 9, Appli	821	58.5	4.8	1012	2	US-09-170-496D-278	Sequence 278, App
749	58.5	4.8	163	4	US-09-489-039A-12148	Sequence 12148, A	822	58.5	4.8	1025	2	US-08-475-891A-4	Sequence 4, Appli
750	58.5	4.8	163	2	US-08-828-832-4	Sequence 4, Appli	823	58.5	4.8	1025	2	US-08-567-375-4	Sequence 4, Appli
751	58.5	4.8	174	4	US-09-270-767-46993	Sequence 46993, A	824	58.5	4.8	1026	2	US-08-587-680A-4	Sequence 4, Appli
752	58.5	4.8	180	4	US-09-270-767-38798	Sequence 38798, A	825	58.5	4.8	1065	2	US-09-623-551-18	Sequence 18, Appl
753	58.5	4.8	180	4	US-09-270-767-54015	Sequence 54015, A	826	58.5	4.8	1274	1	US-08-325-547-3	Sequence 3, Appli
754	58.5	4.8	189	4	US-09-107-532A-7245	Sequence 7245, Ap	827	58.5	4.8	1765	3	US-09-341-587-3	Sequence 3, Appli
755	58.5	4.8	198	3	US-08-737-248-6	Sequence 6, Appli	828	58.5	4.8	1912	1	US-08-409-995-4	Sequence 4, Appli
756	58.5	4.8	226	1	US-08-505-058-6	Sequence 26, Appl	829	58.5	4.8	1912	3	US-08-685-467-4	Sequence 4, Appli
757	58.5	4.8	226	2	US-08-459-818-26	Sequence 26, Appl	830	58.5	4.8	1964	3	US-09-467-997-1	Sequence 1, Appli

831	58.5	4.8	2353	3	US-09-377-155-33	Sequence 33, Appl	504	58	4.8	865	4	US-08-842-382-2	Sequence 2, Appl
832	58.5	4.8	2353	3	US-08-913-942-4	Sequence 4, Appl	505	58	4.8	865	4	US-09-608-821-2	Sequence 2, Appl
833	58.5	4.8	2353	3	US-09-669-974-33	Sequence 33, Appl	506	58	4.8	865	4	US-09-252-991A-23202	Sequence 23202, A
834	58.5	4.8	2353	4	US-09-797-862-33	Sequence 33, Appl	507	58	4.8	1051	4	US-09-252-991A-16989	Sequence 16989, A
835	58.5	4.8	2353	4	US-09-684-707-4	Sequence 4, Appl	508	58	4.8	1122	4	US-09-489-039A-8554	Sequence 8554, Ap
836	58.5	4.8	2354	3	US-09-268-347-47	Sequence 47, Appl	509	58	4.8	1872	6	5386025-6	Patent No. 5386025
837	58.5	4.8	2411	3	US-09-268-347-36	Sequence 36, Appl	510	58	4.8	1873	1	US-08-435-675B-4	Sequence 4, Appl
838	58	4.8	125	4	US-09-248-796A-26907	Sequence 26907, A	511	58	4.8	1873	1	US-08-336-257A-7	Sequence 7, Appl
839	58	4.8	140	4	US-09-270-767-23237	Sequence 33237, A	512	58	4.8	1968	1	US-08-455-543A-45	Sequence 45, Appl
840	58	4.8	170	4	US-09-107-532A-5197	Sequence 5197, Ap	513	58	4.8	1968	2	US-08-223-105C-45	Sequence 45, Appl
841	58	4.8	178	4	US-09-809-665A-12	Sequence 12, Appl	514	58	4.8	2261	4	US-09-526-193A-1	Sequence 1, Appl
842	58	4.8	199	3	US-08-737-248-2	Sequence 2, Appl	515	58	4.8	2539	3	US-09-413-814-42	Sequence 42, Appl
843	58	4.8	199	3	US-08-737-248-11	Sequence 11, Appl	516	57.5	4.7	86	4	US-09-621-976-7127	Sequence 7127, Ap
844	58	4.8	213	3	US-08-397-411-12	Sequence 12, Appl	517	57.5	4.7	99	4	US-09-513-999C-4517	Sequence 4517, Ap
845	58	4.8	225	4	US-09-270-767-40689	Sequence 40689, A	518	57.5	4.7	115	1	US-08-053-131-179	Sequence 179, App
846	58	4.8	225	4	US-09-270-767-55905	Sequence 55905, A	519	57.5	4.7	115	2	US-08-096-762-179	Sequence 179, App
847	58	4.8	234	3	US-08-944-483-46	Sequence 46, Appl	520	57.5	4.7	115	3	US-09-042-353-42	Sequence 42, Appl
848	58	4.8	239	2	US-08-916-902A-1	Sequence 1, Appl	521	57.5	4.7	115	3	US-08-758-417A-307	Sequence 307, App
849	58	4.8	239	2	US-09-213-389-1	Sequence 1, Appl	522	57.5	4.7	122	4	US-09-248-796A-20778	Sequence 2078, A
850	58	4.8	239	2	US-10-164-595-74	Sequence 74, Appl	523	57.5	4.7	141	4	US-09-472-087-88	Sequence 88, Appl
851	58	4.8	254	4	US-09-107-532A-4025	Sequence 4025, A	524	57.5	4.7	143	4	US-09-270-767-33298	Sequence 33298, A
852	58	4.8	288	4	US-09-248-796A-16494	Sequence 16494, A	525	57.5	4.7	157	3	US-09-162-021B-10	Sequence 10, Appl
853	58	4.8	294	4	US-09-710-279-46	Sequence 46, Appl	526	57.5	4.7	163	2	US-08-867-676-1	Sequence 1, Appl
854	58	4.8	315	4	US-09-270-767-33342	Sequence 33342, A	527	57.5	4.7	178	4	US-09-134-000C-4464	Sequence 4464, Ap
855	58	4.8	315	4	US-09-270-767-48539	Sequence 48539, A	528	57.5	4.7	178	4	US-09-248-796A-17314	Sequence 17314, A
856	58	4.8	316	2	US-08-846-762-9	Sequence 9, Appl	529	57.5	4.7	196	4	US-09-710-279-2014	Sequence 2014, Ap
857	58	4.8	316	4	US-09-393-634-39	Sequence 39, Appl	530	57.5	4.7	202	4	US-09-248-796A-26605	Sequence 26605, A
858	58	4.8	348	4	US-09-248-796A-14883	Sequence 14883, A	531	57.5	4.7	205	6	5273901-5	Patent No. 5273901
859	58	4.8	386	4	US-09-107-532A-4764	Sequence 4764, Ap	532	57.5	4.7	222	4	US-09-270-767-41682	Sequence 41682, A
860	58	4.8	401	2	US-08-805-118-1	Sequence 1, Appl	533	57.5	4.7	222	4	US-09-270-767-56927	Sequence 56927, A
861	58	4.8	401	3	US-09-391-958-1	Sequence 1, Appl	534	57.5	4.7	241	4	US-09-270-767-61882	Sequence 61882, A
862	58	4.8	418	4	US-09-252-991A-30786	Sequence 30786, A	535	57.5	4.7	241	4	US-09-248-796A-21158	Sequence 21158, A
863	58	4.8	426	3	US-08-737-248-4	Sequence 4, Appl	536	57.5	4.7	252	4	US-09-134-000C-3729	Sequence 3729, Ap
864	58	4.8	426	4	US-08-311-731A-109	Sequence 109, App	537	57.5	4.7	269	3	US-08-965-056-24	Sequence 24, Appl
865	58	4.8	445	4	US-09-252-991A-28655	Sequence 28655, A	538	57.5	4.7	269	3	US-08-965-056-47	Sequence 47, Appl
866	58	4.8	446	4	US-09-489-039A-7920	Sequence 7920, Ap	539	57.5	4.7	272	4	US-09-270-767-46084	Sequence 46084, A
867	58	4.8	448	1	US-08-366-779-5	Sequence 5, Appl	540	57.5	4.7	293	2	US-08-810-572A-2	Sequence 2, Appl
868	58	4.8	448	1	US-08-789-934-5	Sequence 5, Appl	541	57.5	4.7	293	3	US-09-290-333-2	Sequence 2, Appl
869	58	4.8	448	3	US-08-934-354-5	Sequence 5, Appl	542	57.5	4.7	293	4	US-09-782-857A-2	Sequence 2, Appl
870	58	4.8	448	4	US-09-685-775-5	Sequence 5, Appl	543	57.5	4.7	293	4	US-09-879-919-22	Sequence 22, Appl
871	58	4.8	448	4	US-09-583-110-4257	Sequence 4257, Ap	544	57.5	4.7	293	4	US-09-848-295-4	Sequence 4, Appl
872	58	4.8	459	4	US-09-526-309B-1	Sequence 1, Appl	545	57.5	4.7	293	4	US-09-854-864-14	Sequence 14, Appl
873	58	4.8	467	4	US-09-489-039A-9693	Sequence 9693, Ap	546	57.5	4.7	309	3	US-09-422-869-20	Sequence 20, Appl
874	58	4.8	469	4	US-09-252-991A-26991	Sequence 26991, A	547	57.5	4.7	313	4	US-09-489-847-318	Sequence 318, App
875	58	4.8	485	1	US-08-055-797-2	Sequence 2, Appl	548	57.5	4.7	323	3	US-08-706-281A-12	Sequence 12, Appl
876	58	4.8	485	1	US-07-914-284A-7	Sequence 7, Appl	549	57.5	4.7	323	3	US-09-097-231-12	Sequence 12, Appl
877	58	4.8	485	1	US-08-453-956-15	Sequence 15, Appl	550	57.5	4.7	323	4	US-09-353-099-12	Sequence 12, Appl
878	58	4.8	485	1	US-08-086-631-15	Sequence 15, Appl	551	57.5	4.7	339	4	US-09-690-454-66	Sequence 66, Appl
879	58	4.8	485	2	US-08-452-930-15	Sequence 15, Appl	552	57.5	4.7	340	4	US-09-690-454-174	Sequence 174, App
880	58	4.8	485	5	PCT-US93-08174-15	Sequence 15, Appl	553	57.5	4.7	341	4	US-09-369-247-132	Sequence 132, App
881	58	4.8	486	2	US-08-942-423-2	Sequence 2, Appl	554	57.5	4.7	345	4	US-09-489-039A-9451	Sequence 9471, Ap
882	58	4.8	486	2	US-08-942-423-3	Sequence 3, Appl	555	57.5	4.7	362	3	US-09-146-980-2	Sequence 2, Appl
883	58	4.8	486	3	US-08-630-915A-26	Sequence 26, Appl	556	57.5	4.7	431	4	US-09-866-028-83	Sequence 83, Appl
884	58	4.8	486	4	US-09-879-957-26	Sequence 26, Appl	557	57.5	4.7	431	4	US-09-944-457-83	Sequence 83, Appl
885	58	4.8	486	4	US-09-538-092-926	Sequence 926, App	558	57.5	4.7	443	1	US-09-610-906-1	Sequence 1, Appl
886	58	4.8	504	4	US-09-919-497-67	Sequence 67, App	559	57.5	4.7	455	1	US-08-035-928-2	Sequence 2, Appl
887	58	4.8	519	4	US-09-248-796A-14534	Sequence 14534, A	560	57.5	4.7	470	2	US-08-724-394A-10	Sequence 10, Appl
888	58	4.8	539	4	US-09-252-991A-33061	Sequence 33061, A	561	57.5	4.7	472	4	US-09-489-039A-8418	Sequence 8418, Ap
889	58	4.8	559	4	US-09-583-110-4273	Sequence 4273, Ap	562	57.5	4.7	482	4	US-09-107-532A-4868	Sequence 4868, Ap
890	58	4.8	593	3	US-09-489-039A-13918	Sequence 13918, A	563	57.5	4.7	490	4	US-09-489-039A-13326	Sequence 1326, A
891	58	4.8	593	3	US-09-000-145-4	Sequence 4, Appl	564	57.5	4.7	522	4	US-09-198-452A-480	Sequence 480, App
892	58	4.8	598	4	US-09-198-452A-511	Sequence 511, App	565	57.5	4.7	545	5	US-09-270-767-61684	Sequence 61684, A
893	58	4.8	607	1	US-07-959-943-7	Sequence 7, Appl	566	57.5	4.7	577	6	5310678-3	Patent No. 5310678
894	58	4.8	607	1	US-07-879-617A-12	Sequence 12, Appl	567	57.5	4.7	612	4	US-09-583-110-2911	Sequence 2911, Ap
895	58	4.8	607	1	US-08-753-985-12	Sequence 12, Appl	568	57.5	4.7	658	4	US-09-538-092-1190	Sequence 1190, Ap
896	58	4.8	630	1	US-07-959-943-9	Sequence 9, Appl	569	57.5	4.7	670	4	US-09-134-000C-4606	Sequence 4606, Ap
897	58	4.8	633	3	US-09-041-991A-10	Sequence 10, Appl	570	57.5	4.7	693	4	US-10-140-002-406	Sequence 406, App
898	58	4.8	644	3	US-09-608-533A-10	Sequence 10, Appl	571	57.5	4.7	722	4	US-09-252-991A-17407	Sequence 17407, A
899	58	4.8	644	3	US-09-300-509-18	Sequence 18, Appl	572	57.5	4.7	771	3	US-08-434-000A-8	Sequence 8, Appl
900	58	4.8	651	4	US-09-252-991A-18065	Sequence 18065, A	573	57.5	4.7	771	3	US-09-312-157-8	Sequence 8, Appl
901	58	4.8	653	1	US-07-782-298-2	Sequence 2, Appl	574	57.5	4.7	803	3	US-09-543-681A-4312	Sequence 4312, Ap
902	58	4.8	768	1	US-08-454-455-4	Sequence 4, Appl	575	57.5	4.7	804	4	US-09-116-676-10	Sequence 10, Appl
903	58	4.8	789	3	US-08-727-308-1	Sequence 1, Appl	576	57.5	4.7	896	2	US-08-640-389A-10	Sequence 10, Appl

977	57.5	4.7	896	3	US-08-618-957A-10	Sequence 10, Appl	1050	57	4.7	224	4	US-09-456-090A-46	Sequence 46, Appl
978	57.5	4.7	896	4	US-09-043-816E-13	Sequence 13, Appl	1051	57	4.7	224	4	US-09-453-234-46	Sequence 46, Appl
979	57.5	4.7	896	4	US-09-357-914-33	Sequence 33, Appl	1051	57	4.7	221	4	US-09-134-000C-5609	Sequence 5609, Ap
980	57.5	4.7	896	4	US-08-780-562-3	Sequence 3, Appl	1053	57	4.7	237	4	US-09-270-767-44305	Sequence 44305, A
981	57.5	4.7	896	4	US-09-270-767-46130	Sequence 46130, A	1054	57	4.7	239	3	US-09-134-001C-4165	Sequence 4165, Ap
982	57.5	4.7	898	2	US-08-693-697-36	Sequence 36, Appl	1055	57	4.7	221	4	US-09-252-991A-19334	Sequence 19334, A
983	57.5	4.7	898	4	US-08-588-189-3	Sequence 3, Appl	1056	57	4.7	231	5	PCT-US96-0131A-59	Sequence 59, Appl
984	57.5	4.7	906	2	US-08-640-389A-9	Sequence 9, Appl	1057	57	4.7	229	3	US-08-484-905-117	Sequence 117, App
985	57.5	4.7	906	3	US-08-618-957A-9	Sequence 9, Appl	1058	57	4.7	229	3	US-08-481-985A-117	Sequence 117, App
986	57.5	4.7	906	4	US-09-357-914-32	Sequence 33, Appl	1059	57	4.7	229	3	US-08-370-476-117	Sequence 117, App
987	57.5	4.7	908	2	US-08-693-697-33	Sequence 33, Appl	1060	57	4.7	229	3	US-09-117-853-6	Sequence 6, Appl
988	57.5	4.7	908	2	US-08-588-526-3	Sequence 3, Appl	1061	57	4.7	229	4	US-09-911-154-6	Sequence 6, Appl
989	57.5	4.7	923	4	US-08-780-562-4	Sequence 4, Appl	1062	57	4.7	239	4	US-09-911-514-6	Sequence 6, Appl
990	57.5	4.7	958	2	US-08-640-389A-8	Sequence 8, Appl	1063	57	4.7	223	1	US-08-565-386-13	Sequence 13, Appl
991	57.5	4.7	958	2	US-08-618-957A-8	Sequence 8, Appl	1064	57	4.7	224	4	US-09-489-039A-10177	Sequence 10177, A
992	57.5	4.7	960	1	US-08-355-888A-8	Sequence 8, Appl	1065	57	4.7	227	4	US-09-134-000C-6206	Sequence 6206, Ap
993	57.5	4.7	960	2	US-08-588-190-3	Sequence 3, Appl	1066	57	4.7	270	4	US-09-270-767-37691	Sequence 37691, A
994	57.5	4.7	960	2	US-08-693-697-8	Sequence 8, Appl	1067	57	4.7	270	4	US-09-270-767-52908	Sequence 52908, A
995	57.5	4.7	960	2	US-08-640-389A-3	Sequence 3, Appl	1068	57	4.7	276	4	US-09-110-279-1482	Sequence 1482, Ap
996	57.5	4.7	960	3	US-08-693-696-8	Sequence 8, Appl	1069	57	4.7	232	4	US-09-107-532B-5310	Sequence 5310, Ap
997	57.5	4.7	960	4	US-08-618-957A-3	Sequence 3, Appl	1070	57	4.7	305	4	US-09-489-039A-14056	Sequence 14056, A
998	57.5	4.7	960	4	US-09-357-914-8	Sequence 8, Appl	1071	57	4.7	312	4	US-09-489-039A-13269	Sequence 13269, A
999	57.5	4.7	973	4	US-09-430-723-2	Sequence 2, Appl	1072	57	4.7	323	2	US-08-044-812A-4	Sequence 4, Appl
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1001	57.5	4.7	993	1	US-08-252-517-4	Sequence 4, Appl	1074	57	4.7	333	3	US-09-191-359-4	Sequence 4, Appl
1002	57.5	4.7	993	1	US-08-183-211-2	Sequence 2, Appl	1075	57	4.7	345	5	PCT-US93-0852B-43	Sequence 43, Appl
1003	57.5	4.7	993	1	US-07-906-397A-4	Sequence 4, Appl	1076	57	4.7	352	4	US-09-489-039A-9155	Sequence 9155, Ap
1004	57.5	4.7	993	1	US-08-222-299-4	Sequence 4, Appl	1077	57	4.7	352	4	US-08-698-988A-29	Sequence 29, Appl
1005	57.5	4.7	993	1	US-08-601-691-4	Sequence 4, Appl	1078	57	4.7	359	2	US-08-693-696A-4	Sequence 4, Appl
1006	57.5	4.7	993	2	US-09-021-324-4	Sequence 4, Appl	1079	57	4.7	359	2	US-08-023-610-4	Sequence 4, Appl
1007	57.5	4.7	993	2	US-08-434-878-4	Sequence 4, Appl	1080	57	4.7	359	2	US-08-288-065A-4	Sequence 4, Appl
1008	57.5	4.7	993	4	US-09-872-136B-4	Sequence 4, Appl	1081	57	4.7	359	2	US-08-362-240A-4	Sequence 2, Appl
1009	57.5	4.7	993	5	PCT-US92-09893-3	Sequence 4, Appl	1082	57	4.7	359	3	US-08-804-3782-2	Sequence 4, Appl
1010	57.5	4.7	993	5	PCT-US95-00176A-2	Sequence 2, Appl	1083	57	4.7	369	5	PCT-US95-1024A-4	Sequence 4, Appl
1011	57.5	4.7	993	5	PCT-US95-03718-4	Sequence 4, Appl	1084	57	4.7	374	4	US-09-248-796A-1283	Sequence 1283, A
1012	57.5	4.7	1041	1	US-08-494-714-2	Sequence 2, Appl	1085	57	4.7	376	4	US-09-921-870-44	Sequence 44, Appl
1013	57.5	4.7	1041	5	PCT-US96-10782-2	Sequence 2, Appl	1086	57	4.7	333	3	US-08-749-816-4	Sequence 4, Appl
1014	57.5	4.7	1061	5	US-09-328-352-4445	Sequence 4445, Ap	1087	57	4.7	333	3	US-09-144-914-7	Sequence 7, Appl
1015	57.5	4.7	1160	5	PCT-US92-05401-4	Sequence 4, Appl	1088	57	4.7	403	4	US-09-252-991A-22238	Sequence 22238, A
1016	57.5	4.7	1165	2	US-08-640-389A-11	Sequence 11, Appl	1089	57	4.7	423	4	US-09-248-796A-18022	Sequence 18022, A
1017	57.5	4.7	1165	2	US-08-599-455B-4	Sequence 4, Appl	1090	57	4.7	423	4	US-09-540-236-3466	Sequence 3466, Ap
1018	57.5	4.7	1165	3	US-09-093-814-1	Sequence 1, Appl	1091	57	4.7	445	4	US-09-248-796A-11266	Sequence 11266, A
1019	57.5	4.7	1165	3	US-09-069-781B-4	Sequence 4, Appl	1092	57	4.7	426	4	US-09-134-001C-3711	Sequence 3711, Ap
1020	57.5	4.7	1165	3	US-08-618-957A-11	Sequence 11, Appl	1093	57	4.7	439	4	US-09-526-3099-7	Sequence 7, Appl
1021	57.5	4.7	1165	3	US-09-137-132-4	Sequence 4, Appl	1094	57	4.7	473	4	US-09-107-532B-5699	Sequence 5699, Ap
1022	57.5	4.7	1165	3	US-08-864-564A-4	Sequence 4, Appl	1095	57	4.7	480	4	US-09-252-991A-17687	Sequence 17687, A
1023	57.5	4.7	1165	4	US-09-094-410-4	Sequence 4, Appl	1096	57	4.7	480	4	US-09-107-532A-6160	Sequence 6160, Ap
1024	57.5	4.7	1165	4	US-08-708-123D-4	Sequence 4, Appl	1097	57	4.7	494	4	US-09-543-681A-7142	Sequence 7142, Ap
1025	57.5	4.7	1165	4	US-08-583-153A-4	Sequence 4, Appl	1098	57	4.7	516	4	US-09-248-796A-16798	Sequence 16798, A
1026	57.5	4.7	1165	4	US-08-570-142D-4	Sequence 4, Appl	1099	57	4.7	522	4	US-09-270-767-61564	Sequence 61564, A
1027	57.5	4.7	1165	4	US-08-780-562-2	Sequence 2, Appl	1100	57	4.7	529	4	US-09-489-039A-8824	Sequence 8824, Ap
1028	57.5	4.7	1165	4	US-08-638-524B-4	Sequence 4, Appl	1101	57	4.7	539	4	US-09-602-787A-136	Sequence 136, App
1029	57.5	4.7	1167	3	US-08-857-076-8	Sequence 48, Appl	1102	57	4.7	545	4	US-09-328-352-6221	Sequence 6221, Ap
1030	57.5	4.7	1221	4	US-08-982-430-2	Sequence 2, Appl	1103	57	4.7	546	4	US-09-107-532A-3981	Sequence 3981, Ap
1031	57.5	4.7	3066	3	US-08-952-127-12	Sequence 12, Appl	1104	57	4.7	559	4	US-09-693-146-2	Sequence 2, Appl
1032	57	4.7	91	4	US-09-248-796A-22642	Sequence 22642, A	1105	57	4.7	552	4	US-09-248-796A-23118	Sequence 23118, A
1033	57	4.7	125	4	US-09-270-767-39542	Sequence 39542, A	1106	57	4.7	560	2	US-08-948-569A-10	Sequence 10, Appl
1034	57	4.7	125	4	US-09-270-767-54759	Sequence 54759, A	1107	57	4.7	560	2	US-09-188-469-10	Sequence 10, Appl
1035	57	4.7	127	4	US-09-252-991A-18412	Sequence 18412, A	1108	57	4.7	560	2	US-09-397-338A-10	Sequence 10, Appl
1036	57	4.7	136	4	US-09-615-192A-293	Sequence 293, App	1109	57	4.7	576	4	US-09-252-991A-26023	Sequence 26023, A
1037	57	4.7	139	1	US-08-466-033-177	Sequence 177, App	1110	57	4.7	594	3	US-09-124-141-15	Sequence 15, Appl
1038	57	4.7	139	2	US-08-444-733-177	Sequence 177, App	1111	57	4.7	594	3	US-09-124-141-23	Sequence 23, Appl
1039	57	4.7	139	2	US-08-464-134-177	Sequence 177, App	1112	57	4.7	638	1	US-08-295-814B-13	Sequence 13, Appl
1040	57	4.7	139	2	US-08-461-361-177	Sequence 177, App	1113	57	4.7	638	1	US-08-240-783B-2	Sequence 2, Appl
1041	57	4.7	139	2	US-08-485-910-177	Sequence 177, App	1114	57	4.7	638	3	US-09-084-813-2	Sequence 2, Appl
1042	57	4.7	164	4	US-09-583-110-2884	Sequence 111, App	1115	57	4.7	638	3	PCT-US92-0966C-2	Sequence 13, Appl
1043	57	4.7	199	3	US-08-737-248-12	Sequence 12, Appl	1117	57	4.7	638	5	US-09-343-361-13	Sequence 13, Appl
1044	57	4.7	203	4	US-09-602-787A-436	Sequence 436, App	1118	57	4.7	710	1	US-09-489-039A-89388	Sequence 8888, Ap
1045	57	4.7	217	3	US-09-134-000C-6287	Sequence 6287, Ap	1119	57	4.7	722	1	US-08-162-809-42	Sequence 22, Appl
1046	57	4.7	221	3	US-09-117-853-4	Sequence 4, Appl	1120	57	4.7	722	1	US-08-162-809-4	Sequence 4, Appl
1047	57	4.7	221	4	US-09-911-154-4	Sequence 4, Appl	1121	57	4.7	797	4	US-09-248-796A-16517	Sequence 16517, A
1048	57	4.7	221	4	US-09-911-154-4	Sequence 4, Appl	1121	57	4.7	798	2	US-07-728-215-30	Sequence 30, Appl
1049	57	4.7	221	4	US-09-911-154-4	Sequence 4, Appl	1122	57	4.7	798	2	US-07-728-215-30	Sequence 30, Appl

1123	57	4.7	798	3	US-08-938-085A-30	Sequence 30, Appl	1196	56.5	4.7	423	3	US-09-134-001C-5210	Sequence 5210, Ap
1124	57	4.7	798	4	US-10-072-844-30	Sequence 30, Appl	1197	56.5	4.7	432	2	US-08-677-049-8	Sequence 8, Appl
1125	57	4.7	798	4	US-10-072-838-30	Sequence 30, Appl	1198	56.5	4.7	437	2	US-09-328-352-1237	Sequence 8337, Ap
1126	57	4.7	798	4	US-10-072-841A-30	Sequence 30, Appl	1199	56.5	4.7	442	4	US-09-248-796A-25369	Sequence 25369, A
1127	57	4.7	798	4	US-10-219-631-30	Sequence 30, Appl	1200	56.5	4.7	445	4	US-09-282-218A-12	Sequence 12, Appl
1128	57	4.7	863	1	US-08-325-547-4	Sequence 4, Appl	1201	56.5	4.7	451	4	US-09-270-767-10751	Sequence 40751, A
1129	57	4.7	958	4	US-09-270-767-46021	Sequence 46021, A	1202	56.5	4.7	451	4	US-09-270-767-55967	Sequence 55967, A
1130	57	4.7	1040	4	US-09-489-039A-13619	Sequence 13619, A	1203	56.5	4.7	453	4	US-09-252-991A-32168	Sequence 32168, A
1131	57	4.7	1447	2	US-08-540-406-19	Sequence 19, Appl	1204	56.5	4.7	456	4	US-09-543-681A-6063	Sequence 6063, Ap
1132	57	4.7	1447	3	US-08-656-055-19	Sequence 19, Appl	1205	56.5	4.7	458	4	US-09-270-767-44777	Sequence 44777, A
1133	57	4.7	1447	3	US-08-954-668-19	Sequence 19, Appl	1206	56.5	4.7	483	4	US-09-328-352-6271	Sequence 6271, Ap
1134	57	4.7	1447	3	US-08-268-140-5	Sequence 5, Appl	1207	56.5	4.7	493	3	US-09-134-001C-5370	Sequence 5370, Ap
1135	57	4.7	1447	4	US-08-918-658-19	Sequence 19, Appl	1208	56.5	4.7	503	3	US-09-134-001C-3096	Sequence 3096, Ap
1136	57	4.7	1447	4	US-09-724-631-19	Sequence 19, Appl	1209	56.5	4.7	505	4	US-09-612-402B-17	Sequence 17, Appl
1137	57	4.7	1447	4	US-08-954-701A-19	Sequence 19, Appl	1210	56.5	4.7	579	4	US-09-543-681A-6665	Sequence 6665, Ap
1138	57	4.7	1447	5	PCT-US95-13233-19	Sequence 19, Appl	1211	56.5	4.7	582	4	US-09-721-870-179	Sequence 179, Ap
1139	57	4.7	1523	3	US-09-182-024A-2	Sequence 2, Appl	1212	56.5	4.7	633	4	US-09-918-309A-26	Sequence 26, Appl
1140	56.5	4.7	76	4	US-09-270-767-35561	Sequence 35561, A	1213	56.5	4.7	643	4	US-09-640-198D-2	Sequence 2, Appl
1141	56.5	4.7	76	4	US-09-270-767-50778	Sequence 50778, A	1214	56.5	4.7	661	4	US-09-198-452A-36	Sequence 36, Appl
1142	56.5	4.7	100	4	US-09-899-896-2	Sequence 2, Appl	1215	56.5	4.7	697	4	US-09-976-594-489	Sequence 489, Ap
1143	56.5	4.7	103	4	US-09-634-238-312	Sequence 312, App	1216	56.5	4.7	697	4	US-09-919-039-200	Sequence 200, App
1144	56.5	4.7	143	4	US-09-248-796A-26060	Sequence 26060, A	1217	56.5	4.7	722	2	US-08-997-080-174	Sequence 174, App
1145	56.5	4.7	192	4	US-09-328-352-7294	Sequence 7294, Ap	1218	56.5	4.7	722	2	US-08-997-362-174	Sequence 174, App
1146	56.5	4.7	201	3	US-09-134-001C-4319	Sequence 4319, Ap	1219	56.5	4.7	722	3	US-09-095-855-174	Sequence 174, App
1147	56.5	4.7	207	4	US-08-811-519-26	Sequence 26, Appl	1220	56.5	4.7	722	3	US-09-324-542-174	Sequence 174, App
1148	56.5	4.7	214	2	US-08-480-753-6	Sequence 6, Appl	1221	56.5	4.7	722	4	US-09-205-426-174	Sequence 174, App
1149	56.5	4.7	214	3	US-09-041-889-11	Sequence 11, Appl	1222	56.5	4.7	789	4	US-09-134-000C-4939	Sequence 4939, Ap
1150	56.5	4.7	214	3	US-08-837-058-11	Sequence 11, Appl	1223	56.5	4.7	820	4	US-09-328-352-5766	Sequence 5766, Ap
1151	56.5	4.7	214	4	US-09-417-264-11	Sequence 11, Appl	1224	56.5	4.7	926	4	US-09-270-767-46443	Sequence 46443, A
1152	56.5	4.7	233	3	US-09-355-166-20	Sequence 20, Appl	1225	56.5	4.7	968	4	US-09-270-767-45724	Sequence 45724, A
1153	56.5	4.7	233	4	US-09-270-767-42811	Sequence 42811, A	1226	56.5	4.7	982	4	US-09-556-877-176	Sequence 176, App
1154	56.5	4.7	235	4	US-09-252-991A-18300	Sequence 18300, A	1227	56.5	4.7	982	4	US-09-620-412C-176	Sequence 176, App
1155	56.5	4.7	245	4	US-08-469-260A-40	Sequence 40, Appl	1228	56.5	4.7	982	4	US-09-598-419-176	Sequence 176, App
1156	56.5	4.7	245	4	US-08-468-446-40	Sequence 40, Appl	1229	56.5	4.7	984	4	US-09-612-402B-43	Sequence 43, Appl
1157	56.5	4.7	245	4	US-08-467-344A-40	Sequence 40, Appl	1230	56.5	4.7	1006	4	US-09-556-877-190	Sequence 190, App
1158	56.5	4.7	245	4	US-08-424-550B-40	Sequence 40, Appl	1231	56.5	4.7	1006	4	US-09-620-412C-190	Sequence 190, App
1159	56.5	4.7	249	4	US-09-270-767-56701	Sequence 56701, A	1232	56.5	4.7	1006	4	US-09-598-419-190	Sequence 190, App
1160	56.5	4.7	254	2	US-08-475-427-1	Sequence 1, Appl	1233	56.5	4.7	1012	4	US-09-612-402B-2	Sequence 2, Appl
1161	56.5	4.7	254	4	US-07-842-165-1	Sequence 1, Appl	1234	56.5	4.7	1212	3	US-09-090-535-2	Sequence 2, Appl
1162	56.5	4.7	254	3	US-08-448-398-3	Sequence 3, Appl	1235	56.5	4.7	1212	3	US-09-090-535-2	Sequence 2, Appl
1163	56.5	4.7	277	3	US-09-186-276B-34	Sequence 34, Appl	1236	56.5	4.7	1212	3	US-09-090-535-3	Sequence 3, Appl
1164	56.5	4.7	277	4	US-08-842-445-34	Sequence 34, Appl	1237	56.5	4.7	1212	3	US-09-090-535-4	Sequence 4, Appl
1165	56.5	4.7	277	4	US-09-186-188B-34	Sequence 34, Appl	1238	56.5	4.7	2237	1	US-08-455-543A-48	Sequence 48, Appl
1166	56.5	4.7	292	4	US-09-107-532A-4091	Sequence 4091, Ap	1239	56.5	4.7	2237	2	US-08-223-305C-48	Sequence 48, Appl
1167	56.5	4.7	299	2	US-08-997-080-124	Sequence 124, App	1240	56.5	4.7	2237	3	US-09-268-163-8	Sequence 8, Appl
1168	56.5	4.7	299	2	US-08-997-362-124	Sequence 124, App	1241	56.5	4.7	2261	4	US-09-032-438C-118	Sequence 118, App
1169	56.5	4.7	299	3	US-09-095-885-124	Sequence 124, App	1242	56.5	4.7	2337	3	US-08-713-118-2	Sequence 2, Appl
1170	56.5	4.7	299	3	US-09-324-542-124	Sequence 124, App	1243	56.5	4.7	2337	1	US-09-452-007-2	Sequence 2, Appl
1171	56.5	4.7	299	4	US-09-205-426-124	Sequence 124, App	1244	56.5	4.7	2339	1	US-08-455-543A-47	Sequence 47, Appl
1172	56.5	4.7	300	4	US-09-170-496D-250	Sequence 250, App	1245	56.5	4.7	2339	2	US-08-223-305C-47	Sequence 47, Appl
1173	56.5	4.7	300	4	US-09-170-496D-272	Sequence 272, App	1246	56.5	4.7	2339	3	US-09-268-163-6	Sequence 6, Appl
1174	56.5	4.7	305	4	US-09-270-767-36407	Sequence 36407, A	1247	56.5	4.7	2343	3	US-09-268-163-4	Sequence 4, Appl
1175	56.5	4.7	305	4	US-09-270-767-51624	Sequence 51624, A	1248	56.5	4.7	2396	1	US-08-157-005-2	Sequence 2, Appl
1176	56.5	4.7	307	4	US-09-904-615-142	Sequence 142, App	1249	56.5	4.7	2396	3	US-08-747-863-2	Sequence 2, Appl
1177	56.5	4.7	323	2	US-09-248-796A-20507	Sequence 20507, A	1250	56.5	4.7	2396	4	US-09-565-864-2	Sequence 2, Appl
1178	56.5	4.7	329	2	US-08-475-427-13	Sequence 13, Appl	1251	56	4.6	83	4	US-09-252-991A-24882	Sequence 24882, A
1179	56.5	4.7	329	2	US-07-842-165-13	Sequence 13, Appl	1252	56	4.6	87	4	US-09-134-000C-5199	Sequence 5199, Ap
1180	56.5	4.7	343	2	US-09-328-352-5999	Sequence 5999, Ap	1253	56	4.6	102	3	US-08-984-295-3	Sequence 3, Appl
1181	56.5	4.7	345	4	US-08-446-345-40	Sequence 40, Appl	1254	56	4.6	102	3	US-08-741-411-12	Sequence 12, Appl
1182	56.5	4.7	345	4	US-09-270-767-41480	Sequence 41480, A	1255	56	4.6	105	4	US-09-621-976-5716	Sequence 5716, Ap
1183	56.5	4.7	345	4	US-09-248-796A-15027	Sequence 15027, A	1256	56	4.6	108	3	US-08-974-549A-147	Sequence 147, App
1184	56.5	4.7	346	4	US-09-710-279-504	Sequence 504, App	1257	56	4.6	108	4	US-09-402-181B-147	Sequence 147, App
1185	56.5	4.7	348	4	US-09-270-767-33233	Sequence 43233, A	1258	56	4.6	108	4	US-09-721-456-147	Sequence 147, App
1186	56.5	4.7	348	4	US-09-270-767-44839	Sequence 44839, A	1259	56	4.6	137	4	US-09-252-991A-25510	Sequence 25510, A
1187	56.5	4.7	355	4	US-09-328-352-3374	Sequence 4754, Ap	1260	56	4.6	153	4	US-09-583-110-5135	Sequence 5135, Ap
1188	56.5	4.7	358	4	US-09-543-681A-4765	Sequence 4765, Ap	1261	56	4.6	177	4	US-09-489-039A-10254	Sequence 10254, A
1189	56.5	4.7	359	2	US-08-976-074-5	Sequence 5, Appl	1262	56	4.6	205	4	US-09-540-236-2955	Sequence 2955, Ap
1190	56.5	4.7	359	3	US-08-083-741-5	Sequence 5, Appl	1263	56	4.6	207	4	US-09-252-991A-32255	Sequence 32255, A
1191	56.5	4.7	359	3	US-08-976-166A-5	Sequence 5, Appl	1264	56	4.6	222	4	US-09-302-626B-176	Sequence 176, App
1192	56.5	4.7	363	3	US-09-252-991A-26018	Sequence 26018, A	1265	56	4.6	230	4	US-09-583-110-5271	Sequence 5271, Ap
1193	56.5	4.7	373	3	US-09-134-001C-4029	Sequence 4029, Ap	1266	56	4.6	264	3	US-09-724-864-64	Sequence 64, Appl
1194	56.5	4.7	383	4	US-09-710-279-2026	Sequence 2026, Ap	1267	56	4.6	265	4	US-09-198-452A-1057	Sequence 1057, Ap
1195	56.5	4.7	409	4	US-09-252-991A-19033	Sequence 19033, A	1268	56	4.6	268	4	US-09-134-000C-5310	Sequence 5310, Ap

1269	56	4.6	274	4	US-09-270-767-34307	Sequence 34307, A	1342	56	4.6	755	3	US-08-374-077C-3	Sequence 3, Appl1
1270	56	4.6	274	4	US-09-270-767-49524	Sequence 49524, A	1343	56	4.6	755	3	US-08-895-590-3	Sequence 3, Appl1
1271	56	4.6	275	2	US-08-392-625-17	Sequence 17, Appl1	1344	56	4.6	755	4	US-09-539-879A-3	Sequence 3, Appl1
1272	56	4.6	275	2	US-08-466-961A-17	Sequence 17, Appl1	1345	56	4.6	832	4	US-09-489-039A-12438	Sequence 12438, A
1273	56	4.6	282	4	US-09-107-632A-5553	Sequence 5553, Ap	1346	56	4.6	839	2	US-08-359-705E-6	Sequence 6, Appl1
1274	56	4.6	289	4	US-09-007-288E-145	Sequence 145, App	1347	56	4.6	839	2	US-08-286-846A-6	Sequence 6, Appl1
1275	56	4.6	302	4	US-09-710-279-2980	Sequence 280, Ap	1348	56	4.6	839	2	US-08-457-880A-6	Sequence 6, Appl1
1276	56	4.6	306	1	US-08-414-926A-16	Sequence 16, Appl	1349	56	4.6	839	2	US-08-444-622A-6	Sequence 6, Appl1
1277	56	4.6	306	2	US-08-926-922-16	Sequence 16, Appl	1350	56	4.6	839	3	US-08-942-562-6	Sequence 6, Appl1
1278	56	4.6	306	3	US-09-253-682-16	Sequence 16, Appl	1351	56	4.6	839	3	US-09-156-923-3	Sequence 6, Appl1
1279	56	4.6	306	3	US-09-527-657-16	Sequence 16, Appl	1352	56	4.6	842	5	PCT-US96-02331-15	Sequence 15, Appl
1280	56	4.6	307	4	US-09-852-100-16	Sequence 16, Appl	1353	56	4.6	850	1	US-08-286-305A-7	Sequence 7, Appl1
1281	56	4.6	307	4	US-09-328-352-1994	Sequence 4994, Ap	1354	56	4.6	850	2	US-08-441-104A-7	Sequence 7, Appl1
1282	56	4.6	314	4	US-09-248-796A-18699	Sequence 18699, A	1355	56	4.6	850	2	US-08-440-816A-7	Sequence 7, Appl1
1283	56	4.6	331	3	US-09-134-001C-5188	Sequence 5188, Ap	1356	56	4.6	850	3	US-09-417-381A-7	Sequence 7, Appl1
1284	56	4.6	332	4	US-09-489-039A-12580	Sequence 12580, A	1357	56	4.6	854	4	US-09-350-841A-1589	Sequence 1589, Ap
1285	56	4.6	342	4	US-09-248-796A-15115	Sequence 15115, A	1358	56	4.6	856	3	US-08-486-099-103	Sequence 103, App
1286	56	4.6	350	1	US-08-415-751-15	Sequence 15, Appl	1359	56	4.6	856	3	US-08-484-223A-103	Sequence 103, App
1287	56	4.6	350	3	US-09-134-001C-3383	Sequence 3383, Ap	1360	56	4.6	856	3	US-08-919-597-103	Sequence 103, App
1288	56	4.6	355	2	US-08-846-762-93	Sequence 93, Appl	1361	56	4.6	856	3	US-08-919-597-103	Sequence 103, App
1289	56	4.6	357	4	US-09-252-991A-25036	Sequence 25036, A	1362	56	4.6	856	3	US-08-475-668A-103	Sequence 103, App
1290	56	4.6	359	4	US-09-270-767-59191	Sequence 59191, A	1363	56	4.6	856	3	US-08-485-551A-103	Sequence 103, App
1291	56	4.6	380	4	US-09-328-352-5640	Sequence 5640, Ap	1364	56	4.6	856	3	US-08-471-913A-103	Sequence 103, App
1292	56	4.6	392	4	US-09-491-577-90	Sequence 90, Appl	1365	56	4.6	856	3	US-08-485-264A-103	Sequence 103, App
1293	56	4.6	402	3	US-08-846-704-4	Sequence 4, Appl1	1366	56	4.6	856	4	US-08-474-349A-103	Sequence 103, App
1294	56	4.6	419	3	US-09-948-774-2	Sequence 2, Appl1	1367	56	4.6	856	4	US-08-470-896-103	Sequence 103, App
1295	56	4.6	425	3	US-09-479-128-2	Sequence 2, Appl1	1368	56	4.6	857	1	US-08-220-151-10	Sequence 10, Appl
1296	56	4.6	435	4	US-09-252-991A-17750	Sequence 17750, A	1369	56	4.6	857	1	US-08-413-118-10	Sequence 10, Appl
1297	56	4.6	439	4	US-09-724-797-86	Sequence 86, Appl	1370	56	4.6	857	3	US-08-804-439A-18	Sequence 18, Appl
1298	56	4.6	446	2	US-08-833-610-5	Sequence 5, Appl1	1371	56	4.6	857	3	US-08-360-107A-113	Sequence 113, App
1299	56	4.6	446	3	US-08-834-033A-15	Sequence 15, Appl	1372	56	4.6	857	3	US-08-473-446-10	Sequence 10, Appl
1300	56	4.6	446	4	US-09-377-452-5	Sequence 5, Appl1	1373	56	4.6	857	3	US-08-720-229-18	Sequence 18, Appl
1301	56	4.6	451	4	US-09-489-039A-7269	Sequence 7269, Ap	1374	56	4.6	877	4	US-09-165-396-5	Sequence 5, Appl1
1302	56	4.6	459	3	US-09-002-361-6	Sequence 6, Appl1	1375	56	4.6	944	3	US-09-449-285A-2	Sequence 2, Appl1
1303	56	4.6	459	4	US-09-526-309B-41	Sequence 11, Appl	1376	56	4.6	977	4	US-09-134-000C-5553	Sequence 5553, Ap
1304	56	4.6	463	4	US-09-526-309B-41	Sequence 11, Appl	1377	56	4.6	984	1	US-08-257-073-3	Sequence 3, Appl1
1305	56	4.6	470	4	US-09-328-352-7348	Sequence 7348, Ap	1378	56	4.6	984	2	US-08-184-009-120	Sequence 120, Appl
1306	56	4.6	481	3	US-09-002-361-5	Sequence 5, Appl1	1379	56	4.6	984	2	US-08-458-356-120	Sequence 120, App
1307	56	4.6	492	3	US-09-006-636-4	Sequence 4, Appl1	1380	56	4.6	984	2	US-08-460-736-120	Sequence 120, App
1308	56	4.6	492	3	US-09-006-632-4	Sequence 4, Appl1	1381	56	4.6	984	4	US-09-535-370-120	Sequence 120, App
1309	56	4.6	492	3	US-09-325-214-4	Sequence 4, Appl1	1382	56	4.6	984	4	US-09-663-667-120	Sequence 120, App
1310	56	4.6	503	4	US-09-158-452A-784	Sequence 784, App	1383	56	4.6	989	3	US-08-213-419A-2	Sequence 2, Appl1
1311	56	4.6	504	4	US-09-178-093B-28	Sequence 28, Appl	1384	56	4.6	989	3	US-08-213-419B-2	Sequence 2, Appl1
1312	56	4.6	514	3	US-09-370-098-2	Sequence 2, Appl1	1385	56	4.6	1079	3	US-09-136-652-2	Sequence 2, Appl1
1313	56	4.6	530	4	US-09-540-236-2483	Sequence 2483, Ap	1386	56	4.6	1153	4	US-09-362-842-8	Sequence 8, Appl1
1314	56	4.6	531	4	US-09-721-480-7	Sequence 7, Appl1	1387	56	4.6	2336	3	US-09-268-163-10	Sequence 10, Appl
1315	56	4.6	562	3	US-08-851-843A-5	Sequence 5, Appl1	1388	56	4.6	3011	3	US-08-811-566-20	Sequence 20, Appl
1316	56	4.6	562	3	US-08-854-050-5	Sequence 5, Appl1	1389	56	4.6	3011	3	US-08-811-566-20	Sequence 20, Appl
1317	56	4.6	574	3	US-09-430-323-5	Sequence 5, Appl1	1390	56	4.6	3012	3	US-09-034-756-20	Sequence 20, Appl
1318	56	4.6	574	4	US-09-248-796A-20154	Sequence 20154, A	1391	56	4.6	3012	3	US-08-811-566-2	Sequence 2, Appl1
1319	56	4.6	592	3	US-09-000-145-6	Sequence 6, Appl1	1392	55.5	4.6	11.1	4	US-10-101-464A-634	Sequence 634, App
1320	56	4.6	612	2	US-08-359-705B-8	Sequence 8, Appl1	1393	55.5	4.6	117	3	US-09-291-922-12	Sequence 12, Appl
1321	56	4.6	612	2	US-08-286-846A-8	Sequence 8, Appl1	1394	55.5	4.6	119	4	US-09-134-000C-4301	Sequence 4201, Ap
1322	56	4.6	612	2	US-08-457-860A-8	Sequence 8, Appl1	1395	55.5	4.6	123	4	US-09-107-532A-4158	Sequence 4158, Ap
1323	56	4.6	612	3	US-08-444-622A-8	Sequence 8, Appl1	1396	55.5	4.6	142	4	US-09-472-087-19	Sequence 19, Appl
1324	56	4.6	612	3	US-08-942-562-8	Sequence 8, Appl1	1397	55.5	4.6	142	4	US-09-472-087-19	Sequence 19, Appl
1325	56	4.6	612	3	US-09-156-923-8	Sequence 8, Appl1	1398	55.5	4.6	150	2	US-08-867-676-3	Sequence 3, Appl1
1326	56	4.6	615	4	US-09-602-787A-534	Sequence 534, App	1399	55.5	4.6	155	4	US-09-107-532A-5564	Sequence 5264, Ap
1327	56	4.6	615	4	US-09-602-787A-536	Sequence 536, App	1400	55.5	4.6	158	4	US-09-270-767-34354	Sequence 34354, A
1328	56	4.6	622	2	US-08-132-990A-4	Sequence 4, Appl1	1401	55.5	4.6	158	4	US-09-270-767-49571	Sequence 49571, A
1329	56	4.6	622	5	PCT-US92-09382-4	Sequence 4, Appl1	1402	55.5	4.6	165	4	US-09-543-681A-4340	Sequence 4340, App
1330	56	4.6	625	1	US-08-242-689-2	Sequence 2, Appl1	1403	55.5	4.6	168	3	US-09-199-637A-425	Sequence 425, App
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1333	56	4.6	659	4	US-09-198-452A-432	Sequence 432, App	1406	55.5	4.6	213	4	US-09-115-431-12	Sequence 12, Appl
1334	56	4.6	675	1	US-08-386-495-10	Sequence 10, Appl	1407	55.5	4.6	213	4	US-09-328-352-7428	Sequence 7428, Ap
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1337	56	4.6	693	3	US-08-960-048-11	Sequence 11, Appl	1410	55.5	4.6	247	4	US-09-270-767-44616	Sequence 44616, A
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1340	56	4.6	713	4	US-08-849-212-4	Sequence 4, Appl1	1413	55.5	4.6	263	3	US-09-005-299-2	Sequence 2, Appl1
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1416	55.5	4.6	264	3	US-08-461-985B-120	Sequence 120, App
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1418	55.5	4.6	267	3	US-08-965-056-15	Sequence 15, App1
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1420	55.5	4.6	268	3	US-08-965-056-68	Sequence 68, App1
1421	55.5	4.6	278	4	US-09-252-991A-21606	Sequence 21606, A
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1424	55.5	4.6	295	2	US-08-454-267-7	Sequence 7, App1
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1428	55.5	4.6	305	5	PCT-US93-08528-59	Sequence 59, App1
1429	55.5	4.6	308	4	US-09-252-991A-28210	Sequence 28210, A
1430	55.5	4.6	309	4	US-09-489-039A-9660	Sequence 9660, Ap
1431	55.5	4.6	309	4	US-09-489-039A-11448	Sequence 11448, A
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1434	55.5	4.6	333	4	US-09-543-681A-4619	Sequence 4619, Ap
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1436	55.5	4.6	337	4	US-09-543-681A-6463	Sequence 6463, Ap
1437	55.5	4.6	349	4	US-09-134-001C-4519	Sequence 4519, Ap
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1447	55.5	4.6	400	4	US-09-270-767-11765	Sequence 31765, A
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1449	55.5	4.6	429	4	US-09-328-352-4392	Sequence 4392, Ap
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1452	55.5	4.6	441	1	US-08-835-268-56	Sequence 56, App1
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1457	55.5	4.6	444	4	US-09-546-280-2	Sequence 2, App1
1458	55.5	4.6	444	4	US-09-543-681A-5355	Sequence 5355, Ap
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1461	55.5	4.6	477	1	US-08-453-956-35	Sequence 25, App1
1462	55.5	4.6	477	1	US-08-086-631-55	Sequence 25, App1
1463	55.5	4.6	477	2	US-08-452-930-25	Sequence 25, App1
1464	55.5	4.6	477	5	PCT-US93-08174-25	Sequence 15, App1
1465	55.5	4.6	477	5	US-09-134-001C-5065	Sequence 5065, Ap
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1469	55.5	4.6	493	4	US-09-177-349-5	Sequence 5, App1
1470	55.5	4.6	493	4	US-09-540-236-120	Sequence 2120, Ap
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1474	55.5	4.6	500	3	US-09-467-568-10	Sequence 10, App1
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1477	55.5	4.6	511	4	US-09-188-469-12	Sequence 12, App1
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1479	55.5	4.6	515	2	US-08-406-855A-22	Sequence 22, App1
1480	55.5	4.6	515	3	US-09-206-899-92	Sequence 92, App1
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1487	55.5	4.6	569	3	US-09-362-831-9	Sequence 9, App1

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1490	55.5	4.6	574	2	US-08-916-745-7	Sequence 7, Appl1
1491	55.5	4.6	574	2	US-08-663-808-6	Sequence 6, Appl1
1492	55.5	4.6	574	2	US-09-042-929-7	Sequence 7, Appl1
1493	55.5	4.6	574	2	US-08-546-661-7	Sequence 7, Appl1
1494	55.5	4.6	574	2	US-09-042-960-7	Sequence 7, Appl1
1495	55.5	4.6	574	3	US-09-198-650-7	Sequence 7, Appl1
1496	55.5	4.6	574	3	US-09-332-740-6	Sequence 6, Appl1
1497	55.5	4.6	574	3	US-09-042-913-7	Sequence 7, Appl1
1498	55.5	4.6	574	3	US-09-188-496-6	Sequence 6, Appl1
1499	55.5	4.6	574	3	US-09-042-937-7	Sequence 7, Appl1
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ALIGNMENTS

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RESULT 1
US-08-855-261A-1
? Sequence 1, Application US/08855261A
? Patent No. 5922566
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GENERAL INFORMATION:
? APPLICANT: Bandman, Olga
? APPLICANT: Goli, Surya K.
? APPLICANT: Shah, Puri
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN
? NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/855,261A
? FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0298 US
TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
? LENGTH: 197 amino acids
? TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
? LIBRARY: COLN00719
? CLONE: 1634851
US-08-855-261A-1
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Best Local Similarity 26.5%; Pred. No. 2.8e-11;
Matches 61; Conservative 32; Mismatches 91; Indels 46; Gaps 7;
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			Indels	46;
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RESULT 5
US-08-048-700-2
/ Sequence 2, Application US/08048700
/ Patent No. 5597707
/ GENERAL INFORMATION:
/ APPLICANT: Marken, John
/ APPLICANT: Schieven, Gary L.
/ APPLICANT: Helstrom, Ingegerd
/ APPLICANT: Helstrom, Karl E.
/ APPLICANT: Aruffo, Alejandro
/ TITLE OF INVENTION: A Glycoprotein Tumor Associated Antigen
/ TITLE OF INVENTION: Recognized by The Monoclonal Antibody L6, Its
/ Patent No. 5597707
/ TITLE OF INVENTION: Oligonucleotide Sequence and Methods For Their Use
/
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bristol-Myers Squibb Company
/ STREET: 3005 First Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98121
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/048,700
/ FILING DATE: 15-APR-1993
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Poor, Brian W.
/ REGISTRATION NUMBER: 32,928
/ REFERENCE/DOCKET NUMBER: ON0089-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)728-4800
/ TELEFAX: (206)727-3601
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 202 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Colon
/ CELL TYPE: carcinoma
/ CELL LINE: H3347
/
/ US-08-048-700-2
/
/ Query Match 14.0%; Score 170; DB 1; Length 202;
/ Best Local Similarity 27.4%; Pred. No. 2.9e-11;
/ Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;

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SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 476343
US-09-227-224-4

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Best Local Similarity 23.6%; Pred. No. 4e-10;
Matches 53; Conservative 34; Mismatches 92; Indels 46; Gaps 4;

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QY 124 ANCEFSLKINISDIHPESFNLQWPFNDSCADPTGFNKTSDNTMASGWRASSFHFDEENK 183
DB 120 -----KCSDAHGVWNTTFASTEGQYLINSMSKCYEPK 153
QY 184 HRL-IHFSVFLGLLVGLILEVLFGLSQIVYFGICCGVSKRSQ 227
DB 154 HIVEMHTLFSILLAPAAVEFIQLQIVINGMLGGLCGYCCSRQ 198

RESULT 13

US-09-855-288-10
Sequence 10; Application US/09855288
Patent No. 6632617
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surva K.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Streeter, David G.
TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
FILE REFERENCE: PC-0043 CIP
CURRENT APPLICATION NUMBER: US/09/855,288
CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 202
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Genbank ID No. 6632617 9476343
US-09-855-288-10

Query Match 13.2%; Score 160; DB 4; Length 202;
Best Local Similarity 23.6%; Pred. No. 4e-10;
Matches 53; Conservative 34; Mismatches 92; Indels 46; Gaps 4;

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DB 70 MDEEDCCCGCGYENYGRCSMLSSVLAALIGIVSACVIVASIGLAEGP----- 119
QY 124 ANCEFSLKINISDIHPESFNLQWPFNDSCADPTGFNKTSDNTMASGWRASSFHFDEENK 183
DB 120 -----KCSDAHGVWNTTFASTEGQYLINSMSKCYEPK 153
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DB 154 HIVEMHTLFSILLAPAAVEFIQLQIVINGMLGGLCGYCCSRQ 198

RESULT 14

US-08-839-711-1
Sequence 1; Application US/08839711
Patent No. 6033870
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,711
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0270 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY:
CLONE: 2613105
US-08-839-711-1

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DB 121 CRT-----LDGWEXAFE 132
QY 172 --ASSFHPDE-----ENKGRLIHFSVFLGLLVGI--LEVLFGLSQIVYFGICCG 220
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RESULT 15
US-08-669-974-1

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/ Sequence 1, Application US/08689974
/ Patent No. 576732
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Hawking, Phillip R.
/ APPLICANT: Murray, Lynn E.
/ TITLE OF INVENTION: NOVEL HUMAN INDUCED TUMOR PROTEIN
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/689,974
/ FILING DATE: Filed Herewith
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0113 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 344 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: BRAINOT03
/ CLONE: 530522
/ US-08-689-974-1
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QY 64 PATMTSLTARRKACNNRTGWFSLSPFSVITVIGALYCMILSIQALDKPLMCNSPNSN 123
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 133 GASVMSILPRIGF-SQPRSGLOS---SVITV---YTMVLWTSA-----MTNEP---E 175
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
QY 124 ANCFESLAKNI-----SDHPESFNLOWF-----FNDSCAPPTGFNKPTS 162
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 176 TNCNPSILSLIIGYNTTSTVPEKQGVOMHAQGIIGILFLPLCVFYSSIR--TSNNSQVN 233
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
QY 163 NDMTAS-----GWAASSFHPDSEENKRLI-----HFSVFLGLLLV 198
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 234 KLTITSDSESTLIEDGARSDGSLDGDVHRAVDNERDGVITYSYSPFPMFLFLASTLYI 291
| | | | | | | | | | | | | | | | | | | | | |
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Search completed: January 24, 2005, 15:55:14
Job time : 65 secs

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: January 24, 2005, 15:52:13 (Search time 157 Seconds
(without alignments)
533.242 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCEGWTSCNGSFLVLL.....IVIGFLGCLCGVSKRSQIV 229
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
2002273 segs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
Minimum DB seg length: 0
Maximum DB seg length: 2000000000
Post-processing: Minimum Match 00%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: Genesegp1980s:*
2: Genesegp1990s:*
3: Genesegp2000s:*
4: Genesegp2001s:*
5: Genesegp2002s:*
6: Genesegp2003as:*
7: Genesegp2003bs:*
8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AAy66703	standard; protein; 229 AA.			
DE	Membrane-bound protein PRO994.				
PN	WO9963088-A2.				
PD	09-DEC-1999.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 3; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 2					
ID	AAU29122	standard; protein; 229 AA.			
DE	Human PRO polypeptide sequence #99.				
PN	WO200168848-A2.				
PD	20-SEP-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 4; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 3					
ID	AA887549	standard; protein; 229 AA.			
DE	Human PRO994.				
PN	WO200116318-A2.				
PD	08-MAR-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 4; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 4					
ID	AA665226	standard; protein; 229 AA.			
DE	Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.				
PN	WO200073454-A1.				
PD	07-DEC-2000.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 4; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 5					
ID	ABG95874	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein PRO994.				
PN	US200219130-A1.				
PD	29-AUG-2002.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 5; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 6					
ID	ABU58498	standard; protein; 229 AA.			

DE	Human PRO polypeptide #99.				
PN	US2003027272-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 7					
ID	ABU88046	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003032127-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 8					
ID	ABU84361	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein (PRO) #99.				
PN	US2003032112-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 9					
ID	ABR66235	standard; protein; 229 AA.			
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.				
PN	US2003027278-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 10					
ID	ABR5625	standard; protein; 229 AA.			
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.				
PN	US2003036159-A1.				
PD	20-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 11					
ID	ABU9565	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein (PRO) #99.				
PN	US2003040070-A1.				
PD	27-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 12					
ID	ABU58041	standard; protein; 229 AA.			
DE	Human PRO polypeptide #3.				
PN	US2003027163-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 13					
ID	ABU59119	standard; protein; 229 AA.			
DE	Novel human secreted or transmembrane protein PRO994.				
PN	US2002132252-A1.				
PD	19-SEP-2002.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 14					
ID	ABU82631	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein PRO994.				
PN	US2003032023-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 15					
ID	ABU82804	standard; protein; 229 AA.			
DE	Human PRO polypeptide #99.				
PN	US2003032113-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1215; DB 6; Length 229;			
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 16					
ID	ABU89925	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003036147-A1.				

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PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 17
ID ABR6174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 28
ID ABU96051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 30
ID ABU9450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 31
ID ABU66291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 33
ID ABU60532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 36
ID ABO33958 standard; protein; 229 AA.
```

DE Human secreted/transmembrane protein PRO994.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 43
ID ABO11975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 44
ID ABR85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 46
ID ABO11532 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 48
ID ABR88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 49
ID ABR83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

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PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID NO:198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 66
ID ABU6362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.
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PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 67
ID ABU93307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 71
ID ABR6394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.
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PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 78
ID ABR6479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US200302135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 80
ID ABUS9266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 81
ID ABUS371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 82
ID ABUS9061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 83
ID ABUS3141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US200302105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 84
ID ABUS9197 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200302123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 85
ID ABUS90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 86
ID ABUS4056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US200302111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
Query Match 100.0%; Score 1215; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 87
ID ABUS3707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200302119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 94
ID ABUS7029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 95
ID ABUS5981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US20030222100-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 96
ID ABUS2268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 99
ID AB008125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 103
ID ABU91169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 104
ID ABR59629 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 107
ID ABR6540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027252-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 123
ID ABR79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 127
ID ABU90235 standard; protein; 229 AA.

DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
PRED. NO. 3.5e-132;
RESULT 137
ID ABU80133 standard; protein; 229 AA.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 138
ID AB08498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 139
ID AB092181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 140
ID AB093402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 141
ID AB093955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 142
ID AB090940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 143
ID AB096462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 144
ID AB01087 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 145
ID AB010608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 146
ID AB081639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 147

ID AB072132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 148
ID AB095617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 149
ID AB096826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 150
ID AB070671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 151
ID AB005022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 152
ID AB008430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 153
ID AB088578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 154
ID AB034092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 155
ID AB005637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 156
ID AB074026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 157

RESULT 157
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 158
ID ABR00915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 166
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (seqid 48).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 180
ID AM77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 181
ID AM27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 182
ID ABM06155 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 183
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 184
ID ABM35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 185
ID ABM26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 190
ID ABM11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 191
ID ABM02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 192
ID ABM16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 194
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ID ABM29094 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 209
ID ABR30653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 221
ID ABO3352 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 222
ID ABO04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 223
ID ABO08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 227
ID ABO10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 228
ID ABO11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 231
ID ADA1910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 232
ID ABO33719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003052134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 234
ID ADA1786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 241
ID ABM06460 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 247
ID ABM31180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 257
ID AMO1221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 258
ID ABR88823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 260
ID ABM20859 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 267
ID AMW74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 270
ID ABM24441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 271
ID ABR6383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 272
ID ABR6688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 273
ID ABM6652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 276
ID ABM3909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 277
ID ABM33299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US200310061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 298

ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 310
ID ABM77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 312
ID ABM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 326
ID ABO51791 standard; protein; 229 AA.

DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 333
ID ADA36699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 334
ID ABM1255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 336
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003056129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 355
ID ABR73111 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 363
ID ABM1340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 365
ID ABR73111 standard; protein; 229 AA.

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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 365
ID ABO30653 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 367
ID AEM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 368
ID AEM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 369
ID AEM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 371
ID AEM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 375
ID AEM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 383
ID ABM26959 standard; protein; 229 AA.
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DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 390
ID ABR7115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 393
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 403
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 404
ID ABR19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 405
ID ABR19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 414
ID ABR01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 415
ID ABR02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 417
ID ABR12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 418
ID ABR30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 419
ID ABR24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 7; Length 229;
RESULT 421

ID ABO31263 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 422
ID ABM44390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 423
ID ABM09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 425
ID ABM4705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 430
ID ABR7720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 433
ID ABR3788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 434
ID ABM1831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 435
ID ABM78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 438
ID ABM27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 439
ID ABM13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 440
ID ABO31873 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 443
ID ARO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;

Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 465
ID ABO41075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 466
ID ABO36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 467
ID ABO37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 470
ID ABO46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 474
ID ABM1839 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 478
ID ABM32449 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US3003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 03-APR-2003.
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 03-APR-2003.
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 27-MAR-2003.
ID ADB31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 10-APR-2003.
ID ADB30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 10-APR-2003.
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 06-FEB-2003.
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 06-FEB-2003.
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 06-MAR-2003.
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 13-MAR-2003.
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 03-APR-2003.
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 03-APR-2003.
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 03-APR-2003.
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 10-APR-2003.
ID ADC1436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 10-APR-2003.
ID ADC1481 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 17-APR-2003.
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 24-JUL-2003.
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 01-MAY-2003.
ID ADC1494 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 01-MAY-2003.
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 10-APR-2003.
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
PD 01-MAY-2003.
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 498
ID ADG62448 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 499
ID ADD05671 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 500
ID ADD08628 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 501
ID ADD08677 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 502
ID ADC83124 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 503
ID ADD55231 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 504
ID ADD36052 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 505
ID ADD56189 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 506
ID ADD54627 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 507
ID ADE26781 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003077594-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 508
ID ADE26248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 509
ID ADF67185 standard; protein; 229 AA.
DE Human PRO994 amino acid sequence SEQ ID NO:258.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 510
ID ADG01053 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 511
ID ADG08606 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 512
ID ADG02666 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 513
ID ADG01373 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 514
ID ADF95548 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 515
ID ADF95227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 516
ID ADG12363 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;

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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 522
ID ADH85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 527
ID ADH85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 530
ID ADH83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 535
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ID ADH57383 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 544
ID ADI35439 standard; protein; 229 AA.

DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.

Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 572		
ID ADI19441 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181675-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 573		
ID ADI05242 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181677-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 574		
ID ADH79654 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003191288-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 575		
ID ADI01480 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181678-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 576		
ID ADI01650 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181679-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 577		
ID ADI01820 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181680-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 578		
ID ADH79824 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003191289-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 579		
ID ADI04642 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003171550-A1.		
PD 11-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 580		
ID ADI02778 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181651-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 581		
ID ADI02778 standard; protein; 229 AA.		
DE Novel human secreted and transmembrane protein PRO994.		
FN US2003181651-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1215; DB 7; Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;

RESULT 581	ID	ADH78097	standard; protein; 229 AA.
	DE	Human PRO polypeptide #24.	
	PN	US2003181667-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 582	ID	AD125736	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003181670-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 583	ID	AD125906	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003181671-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 584	ID	ADK65418	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003073821-A1.	
	PD	17-APR-2003	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 585	ID	ADH98760	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003191284-A1.	
	PD	09-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 586	ID	ADH80001	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003191287-A1.	
	PD	09-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 587	ID	AD132804	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003207386-A1.	
	PD	06-NOV-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 588	ID	ADM0338	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003073813-A1.	
	PD	17-APR-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 589	ID	AD193732	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003040013-A1.	
	PD	27-FEB-2003	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;
RESULT 590	ID	AD193732	standard; protein; 229 AA.
	DE	Novel human secreted and transmembrane protein PRO094.	
	PN	US2003040013-A1.	
	PD	27-FEB-2003	
	PA	(GETH) GENENTECH INC.	
	Query Match	100.0%;	Score 1215; DB 7; Length 229;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-132;

Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 600				
ID ADG6869 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US200318085-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 601				
ID ADH27759 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180912-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 602				
ID ADH25100 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180913-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 603				
ID ADH33732 standard; protein; 229 AA.				
ID Human PRO polypeptide #24.				
PN US2003181645-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 604				
ID ADG82847 standard; protein; 229 AA.				
ID Human PRO polypeptide #99.				
PN US2003215910-A1.				
PD 20-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 605				
ID ADH02375 standard; protein; 229 AA.				
ID Human PRO polypeptide #24.				
PN US2003180839-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 606				
ID ADH07962 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180845-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 607				
ID ADG69379 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180846-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 608				
ID ADH39200 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 609				
ID ADH39200 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 610				
ID ADH39200 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 611				
ID ADH39200 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 612				
ID ADH39200 standard; protein; 229 AA.				
ID Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				

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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 609
ID ADH25128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 610
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 611
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 612
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 613
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 614
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 615
ID ADG24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 616
ID ADH31097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 617
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 618
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 619
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 620
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 621
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 622
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 623
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 624
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 625
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 626
ID ADH02205 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 627
ID ADG69209 standard; protein; 229 AA.
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DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 628
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 629
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 630
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 631
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 632
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 633
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 634
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 635
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 636
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 637
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 638
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 639
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 640
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 641
ID ADH43567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 642
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 643
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 644
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 645
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 646
ID ADH9699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 647
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 648
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US20031817197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 649
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 650
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 651
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 652
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 653
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 654
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 655
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 656
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 657
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 658
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 659
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 660
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 661
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 662
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 663
ID ABP41230 standard; protein; 205 AA.
DE Human ovarian antigen HSPS174, SEQ ID NO:2362.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 14.3%; Score 173.5; DB 5; Length 205;
Best Local Similarity 27.7%; Pred. No. 3e-11;
RESULT 664
ID AAW61625 standard; protein; 197 AA.
DE Clone HGBGV89 of TM4SF superfamily.
PN MO9831799-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 665
ID AAM88494 standard; protein; 197 AA.
DE Human stomach cancer clone HPO1440-encoded transmembrane protein.
PN MO9855508-A2.
PD 10-DEC-1998.
PA (SAGA-) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 666
ID AAW84273 standard; protein; 197 AA.
DE A tumour associated antigen designated TUAN.
PN MO9851706-A1.
PD 19-NOV-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 667
ID ADD10280 standard; protein; 197 AA.
DE Human tumour-associated antigen, TUAN.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 14.0%; Score 170; DB 7; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 668
ID AAW01507 standard; protein; 197 AA.
DE Human receptor protein from clone HGBGV89.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 14.0%; Score 170; DB 7; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 669
ID ADN41032 standard; protein; 197 AA.
DE Novel human secreted protein seq'd 154.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPE/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAM/) KYAM H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSH C E.
Query Match 14.0%; Score 170; DB 8; Length 197;
Best Local Similarity 26.5%; Pred. No. 7.2e-11;
RESULT 670
ID AAY02732 standard; protein; 198 AA.
DE Human secreted protein encoded by gene 83 clone HGBGV89.
PN MO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 2; Length 198;
Best Local Similarity 26.5%; Pred. No. 7.3e-11;

RESULT 671
ID ADA07411 standard; protein; 198 AA.
DE Human secreted protein from gene 83.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPE/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAM/) KYAM H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match 14.0%; Score 170; DB 7; Length 198;
Best Local Similarity 26.5%; Pred. No. 7.3e-11;
RESULT 672
ID AAW14123 standard; protein; 202 AA.
DE Human tumour-associated L6 antigen.
PN US5597707-A.
PD 28-JAN-1997.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 14.0%; Score 170; DB 2; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 673
ID AAY92049 standard; protein; 202 AA.
DE HRPcA3 polypeptide from androgen-inducible gene clone.
PN WO200018961-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNITIUM PHARM INC.
Query Match 14.0%; Score 170; DB 3; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 674
ID AAB31499 standard; protein; 202 AA.
DE Gene 36 human secreted protein homologous amino acid sequence #167.
PN WO200056755-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 3; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 675
ID ABB68619 standard; protein; 202 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 168.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 14.0%; Score 170; DB 5; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 676
ID ADD10288 standard; protein; 202 AA.
DE human tumour-associated L6antigen.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 677
ID AAW01521 standard; protein; 202 AA.
DE Protein #9 used in the present invention.
PN US2003129696-A1.
PD 10-UTL-2003.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 678
ID ADF61842 standard; protein; 202 AA.
DE Human transmembrane 4 superfamily member 1 protein.

PN WO2003088910-A2.
PD 30-OCT-2003.
PA (RIGB-) RIGEL PHARM INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 679
ID ADK38674 standard; protein; 202 AA.
DE Human prostate cancer associated protein HRPca 3.
PN US200338865-A1.
PD 24-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 680
ID ADN40006 standard; protein; 202 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C376.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 7.5e-11;
RESULT 681
ID ABP68635 standard; protein; 202 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 4558.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (COR-) CORIXA CORP.
Query Match 13.7%; Score 166.5; DB 5; Length 202;
Best Local Similarity 26.7%; Pred. No. 1.9e-10;
RESULT 682
ID ADN3985 standard; protein; 202 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C355.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.7%; Score 166.5; DB 7; Length 202;
Best Local Similarity 26.7%; Pred. No. 1.9e-10;
RESULT 683
ID ADI21569 standard; protein; 209 AA.
DE Novel human polypeptide #48.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 166.5; DB 7; Length 209;
Best Local Similarity 26.7%; Pred. No. 2e-10;
RESULT 684
ID ABW01520 standard; protein; 197 AA.
DE Protein #8 used in the present invention.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 13.7%; Score 166; DB 7; Length 197;
Best Local Similarity 26.1%; Pred. No. 2.1e-10;
RESULT 685
ID ABR61633 standard; protein; 202 AA.
DE LRTM4 protein #SEQ ID 2.
PN CN1367179-A.
PD 04-SEP-2002.
PA (SHNH-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 13.2%; Score 160.5; DB 6; Length 202;
Best Local Similarity 21.6%; Pred. No. 9.5e-10;
RESULT 686
ID ADD10289 standard; protein; 202 AA.
DE Mouse tumour-associated Lcan1gcn.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 13.2%; Score 160; DB 7; Length 202;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 687
ID AAO30178 standard; protein; 132 AA.

DE Human transmembrane 4 super family member 5 splice variant (TW4SFS).
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GENT-) GENSET SA.
Query Match 12.6%; Score 153; DB 6; Length 132;
Best Local Similarity 34.5%; Pred. No. 3.9e-09;
RESULT 688
ID ADI21083 standard; protein; 184 AA.
DE Novel human protein #58.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 147.5; DB 7; Length 184;
Best Local Similarity 25.2%; Pred. No. 2.7e-08;
RESULT 689
ID AAB44087 standard; protein; 153 AA.
DE Human cancer associated protein sequence SEQ ID NO: 1532.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.9%; Score 144; DB 3; Length 153;
Best Local Similarity 33.3%; Pred. No. 5.3e-08;
RESULT 690
ID AAB54023 standard; protein; 245 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO: 475.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.7%; Score 142; DB 3; Length 245;
Best Local Similarity 31.0%; Pred. No. 1.8e-07;
RESULT 691
ID ABB72399 standard; protein; 145 AA.
DE Human protein isolated from skin cells SEQ ID NO: 723.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 11.6%; Score 140.5; DB 5; Length 145;
Best Local Similarity 33.3%; Pred. No. 1.3e-07;
RESULT 692
ID ADD69578 standard; protein; 170 AA.
DE Human REMAP protein - SEQ ID 7.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.4%; Score 138.5; DB 7; Length 170;
Best Local Similarity 24.9%; Pred. No. 2.7e-07;
RESULT 693
ID AAM61626 standard; protein; 201 AA.
DE Clone HUVB80 of TM4SF superfamily.
PN WO9831799-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 126; DB 2; Length 201;
Best Local Similarity 21.8%; Pred. No. 9.6e-06;
RESULT 694
ID ABU03461 standard; protein; 201 AA.
DE Angiogenesis-associated human protein sequence #6.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.4%; Score 126; DB 6; Length 201;
Best Local Similarity 21.8%; Pred. No. 9.6e-06;
RESULT 695
ID ABW01508 standard; protein; 201 AA.
DE Human receptor protein from clone HUVB80.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 10.4%; Score 126; DB 7; Length 201;
Best Local Similarity 21.8%; Pred. No. 9.6e-06;
RESULT 696

ID ADN38692 standard; protein; 201 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:10.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.4%; Score 126; DB 7; Length 201;
Best Local Similarity 21.8%; Pred. No. 9.6e-06;
RESULT 697
ID AAM80948 standard; protein; 205 AA.
DE Amino acid sequence of the human integral membrane protein-2.
PN WO9846752-A1.
PD 22-OCT-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.3%; Score 125; DB 2; Length 205;
Best Local Similarity 21.8%; Pred. No. 1.3e-05;
RESULT 698
ID AAB34200 standard; protein; 202 AA.
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:168.
PN WO200056755-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 122; DB 3; Length 202;
Best Local Similarity 23.2%; Pred. No. 2.8e-05;
RESULT 699
ID AAU30786 standard; protein; 226 AA.
DE Novel human secreted protein #1277.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 121; DB 4; Length 226;
Best Local Similarity 25.5%; Pred. No. 4.3e-05;
RESULT 700
ID AAY12177 standard; protein; 122 AA.
DE Human 5' EST secreted protein SEQ ID NO: 490.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 122;
Best Local Similarity 28.8%; Pred. No. 2.4e-05;
RESULT 701
ID AAY12854 standard; protein; 136 AA.
DE Human 5' EST secreted protein SEQ ID NO:444.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 136;
Best Local Similarity 28.8%; Pred. No. 2.8e-05;
RESULT 702
ID AAY12178 standard; protein; 150 AA.
DE Human 5' EST secreted protein SEQ ID NO: 491.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 150;
Best Local Similarity 28.8%; Pred. No. 3.2e-05;
RESULT 703
ID AAB64612 standard; protein; 108 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 122.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 119.5; DB 4; Length 108;
Best Local Similarity 33.7%; Pred. No. 2.3e-05;
RESULT 704
ID AAB64564 standard; protein; 180 AA.
DE Human secreted protein #16.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 119.5; DB 4; Length 180;
Best Local Similarity 33.7%; Pred. No. 4.7e-05;

RESULT 705
ID ABP76262 standard; protein; 109 AA.
DE Human GENSET protein SEQ ID 812.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST-) GENSET.
Query Match 9.4%; Score 114.5; DB 6; Length 109;
Best Local Similarity 33.3%; Pred. No. 8.8e-05;
RESULT 706
ID AAB64611 standard; protein; 108 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 121.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.3%; Score 113.5; DB 4; Length 108;
Best Local Similarity 33.7%; Pred. No. 0.00011;
RESULT 707
ID AAM64540 standard; protein; 209 AA.
DE Human fibrosarcoma cell line HT-1080 clone HP10034 protein.
PN WO9821338-A2.
PD 22-MAY-1998.
PA (SAGA) SAGAMI CHEM RES CENTRE.
Query Match 9.2%; Score 111.5; DB 2; Length 209;
Best Local Similarity 20.2%; Pred. No. 0.00049;
RESULT 708
ID AAM51208 standard; protein; 209 AA.
DE Human osteoclast expressed polypeptide SEQ ID NO 2.
PN JP2001231573-A.
PD 28-AUG-2001.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 9.2%; Score 111.5; DB 4; Length 209;
Best Local Similarity 20.2%; Pred. No. 0.00049;
RESULT 709
ID AAU29953 standard; protein; 107 AA.
DE Novel human secreted protein #444.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 105; DB 4; Length 107;
Best Local Similarity 31.2%; Pred. No. 0.0011;
RESULT 710
ID ADP66649 standard; protein; 450 AA.
DE Mouse GHB receptor related polypeptide.
PN WO2004046315-A2.
PD 03-JUN-2004.
PA (SLOW-) SLOWAVE INC.
Query Match 8.3%; Score 101; DB 8; Length 450;
Best Local Similarity 23.0%; Pred. No. 0.024;
RESULT 711
ID AAY11655 standard; protein; 86 AA.
DE Human 5' EST secreted protein SEQ ID NO:307.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 7.9%; Score 95.5; DB 2; Length 86;
Best Local Similarity 32.9%; Pred. No. 0.01;
RESULT 712
ID ADP66647 standard; protein; 450 AA.
DE Rat GHB receptor related polypeptide.
PN WO2004046315-A2.
PD 03-JUN-2004.
PA (SLOW-) SLOWAVE INC.
Query Match 7.7%; Score 93; DB 8; Length 450;
Best Local Similarity 23.7%; Pred. No. 0.21;
RESULT 713
ID ABG29044 standard; protein; 426 AA.
DE Novel human diagnostic protein #29035.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 90.5; DB 4; Length 426;

Best Local Similarity 30.8%; Pred. No. 0.37;
RESULT 714
ID ABG24776 standard; protein; 708 AA.
DE Novel human diagnostic protein #24767.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 30.8%; Pred. No. 0.76;
RESULT 715
ID ABG29047 standard; protein; 997 AA.
DE Novel human diagnostic protein #29038.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.4%; Score 90.5; DB 4; Length 708;
Best Local Similarity 30.8%; Pred. No. 1.2;
RESULT 716
ID ABG24324 standard; protein; 1118 AA.
DE Novel human diagnostic protein #24315.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.4%; Score 90.5; DB 4; Length 997;
Best Local Similarity 30.8%; Pred. No. 1.5;
RESULT 717
ID ABU99046 standard; protein; 1036 AA.
DE Protein encoded by Prokaryotic essential gene #34573.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELITRA PHARM INC.
Query Match
Best Local Similarity 7.2%; Score 88; DB 6; Length 1036;
Best Local Similarity 31.5%; Pred. No. 2.6;
RESULT 718
ID ADB65669 standard; protein; 117 AA.
DE Human protein encoded by clone TRACH20011540.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.2%; Score 87.5; DB 7; Length 117;
RESULT 719
ID AAU30827 standard; protein; 185 AA.
DE Novel human secreted protein #118.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.2%; Score 87.5; DB 4; Length 185;
Best Local Similarity 28.1%; Pred. No. 0.25;
RESULT 720
ID ADJ48738 standard; protein; 1174 AA.
DE O11-associated gene related protein #38.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 7.2%; Score 87; DB 8; Length 1174;
Best Local Similarity 20.8%; Pred. No. 4;
RESULT 721
ID ABU99666 standard; protein; 891 AA.
DE Protein encoded by Prokaryotic essential gene #35193.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELITRA PHARM INC.
Query Match
Best Local Similarity 7.1%; Score 86.5; DB 6; Length 891;
Best Local Similarity 22.6%; Pred. No. 3.1;
RESULT 722
ID ABB48024 standard; protein; 283 AA.
DE Listeria monocytogenes protein #728.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INBP) INST PASTEUR.
Query Match
Best Local Similarity 7.1%; Score 86; DB 5; Length 283;
RESULT 723
ID AAM98770 standard; protein; 449 AA.
DE H. pylori GHPO 1130 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.1%; Score 86; DB 2; Length 449;
Best Local Similarity 31.5%; Pred. No. 1.3;
RESULT 724
ID AAY59127 standard; protein; 271 AA.
DE Protein encoded by V. cholerae thyA gene 5' flanking region.
PN WO9961634-A1.
PD 02-DEC-1999.
PA (SBLV-) SBL VACCIN AB.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 3; Length 271;
Best Local Similarity 23.1%; Pred. No. 0.75;
RESULT 725
ID AAM52812 standard; protein; 344 AA.
DE Human induced tumour protein.
PN WO9806846-A1.
PD 19-FEB-1998.
PA (INCYTE PHARM INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 2; Length 344;
Best Local Similarity 23.1%; Pred. No. 1;
RESULT 726
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 2; Length 356;
Best Local Similarity 23.1%; Pred. No. 1.1;
RESULT 727
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 3; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 728
ID AAG65236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 729
ID AAU29065 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 730
ID AAM39489 standard; protein; 453 AA.
DE Human polypeptide seq ID NO 2634.
PN WO200153313-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 731
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.

PN W020073454-A1.
PD 07-DEC-2000.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 4; Length 453;
PD 27-FEB-2003.
RESULT 732
ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 5; Length 453;
RESULT 733
ID ABB58441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 734
ID ABU87989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 735
ID ABU84304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 736
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 737
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 738
ID ABU9508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 739
ID ABU57985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 740
ID ABU59063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2003132252-A1.
PD 19-FEB-2002.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 741
ID ABU82575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 742
ID ABU82747 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 743
ID ABU8968 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 744
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 745
ID ABU60494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 746
ID ABU96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 747
ID ABU92601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 748
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 749
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 750
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 751
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.

Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 752
ID ABU13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 753
ID ABU85619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 754
ID ABU98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003033153-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 755
ID ABU97994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 756
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 757
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 758
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 759
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 760
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 761
ID ABU2461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.

PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 762
ID ABR99393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 763
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 764
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027267-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 765
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 766
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 767
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 768
ID ABU85004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 769
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 770
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 771
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.

PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 772
ID ABU8694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US200303613-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 773
ID ABU8389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US200303613-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 774
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 775
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 776
ID ABO09288 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 777
ID ABO19152 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 778
ID ABO11170 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 779
ID ABR6678 standard; protein; 453 AA.
DE Novel human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 780
ID ABO16001 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 781
ID ABO13707 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 782
ID ABU65610 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, SEQ ID 84.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 783
ID ABO07458 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 784
ID ABO03645 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 785
ID ABR67093 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 786
ID ABO15696 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 787
ID ABUS5977 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 788
ID ABUS5305 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 789
ID ABUS250 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 790
ID ABU71153 standard; protein; 453 AA.
DE Human PRO732 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 791
ID ABO07763 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
RESULT 792

ID ABR70004 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 793
ID ABR69337 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 794
ID ABO01478 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 795
ID ABU81280 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 796
ID ABR60077 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 797
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 798
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 799
ID ABR6422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 800
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 801
ID ABU59210 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 802

ID ABU85314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 803
ID ABU69004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 804
ID ABU83084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 805
ID ABU94940 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 806
ID ABU90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 807
ID ABU83999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 808
ID ABU93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 809
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 810
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 811
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 812
ID ABO06543 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 813
ID ABR9088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 814
ID ABUS6972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 815
ID ABUS924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 816
ID ABUS221 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 817
ID ABUS7222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 818
ID ABUS3694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 819
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 820
ID ABUS1779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 821
ID ABUS6943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 822
ID ABR5772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 823
ID ABUS93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 824
ID ABUS9813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 825
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 826
ID ABR90901 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 827
ID ABUS8916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 828
ID ABUS94328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 829
ID ABUS7210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 830
ID ABUS6539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 831
ID ABUS6644 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;
RESULT 832
ID ABUS94633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;
Pred. No. 1.5;

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Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 833
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 834
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 835
ID ABU92294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 836
ID ABU98474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 837
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 838
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 839
ID ABUS9359 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 840
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 841
ID ABU92906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 842
ID ABU95865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; DB 6; Length 453;
RESULT 843
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
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PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 854
ID ABU93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 855
ID ABO09898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 856
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 857
ID ABU10831 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 858
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 859
ID ABU81583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 860
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 861
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 862
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 863
ID ABO04965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.

PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 864
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 865
ID ABU85522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 866
ID ABO34036 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 867
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 868
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 869
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 870
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 871
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 872
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 873
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 874
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 875
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 876
ID ABO31511 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 877
ID ABM07928 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 878
ID ABO40408 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 879
ID ABO35833 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 880
ID ABO43972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 881
ID ADA77836 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 882
ID ABO35833 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;

ID ABM24767 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 883
ID ABO03035 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 884
ID ABR90291 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 885
ID ABM17205 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 886
ID ABR94951 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 887
ID ABR95256 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 888
ID ABO21494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 889
ID ABR97758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 890
ID ABR87546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;
RESULT 891
ID ABM77587 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
PRED. No. 1.5;

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Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 892
ID ABO27817 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 893
ID ABO26098 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 894
ID ABO2604 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 895
ID ABO2505 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 896
ID ABO26292 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 897
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 898
ID ABO2816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 899
ID ABO2457 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 900
ID ABO437584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 901
ID ABO11588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 902
ID ABO2689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 903
ID ABO15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 904
ID ABO27546 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 905
ID ABO29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 906
ID ABO07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 907
ID ABO21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 908
ID ABO09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 909
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;
RESULT 910
ID ABO27546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 911
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 912
ID ABO76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 913
ID ABO76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 914
ID ABO5662 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 915
ID ABO5987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 916
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 917
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 918
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 919
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 920

ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 921
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 922
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 923
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 924
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 925
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 926
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 927
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 928
ID ABR87851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 929
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 930
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 931
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 932
ID AMO4883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 933
ID AMO8843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 934
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 935
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 936
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 937
ID ABO10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 938
ID ABO11893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 939
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 940
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 941
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 942
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 943
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 944
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 945
ID ABO10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 946
ID ABO28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 947
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No.1.5;
RESULT 948
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ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 949
ID ABM06403 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 950
ID ABM04214 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 951
ID ABM22327 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 952
ID ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 953
ID ABO40713 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 954
ID ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 955
ID ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 956
ID ABO52649 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 957
ID ABO50209 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 958
ID ABU99203 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 959
ID ABO04255 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 960
ID ABO05885 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 961
ID ABM18425 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 962
ID ADA27709 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 963
ID ABR97453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 964
ID ABR80553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 965
ID ABM01164 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 966
ID ABR88766 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 967

ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 969
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 970
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 971
ID ABM10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 972
ID ABO38578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 973
ID ABM32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 974
ID ABM22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 975
ID ABM74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 976
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.

PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 977
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 978
ID ABM02384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 979
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 980
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 981
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 982
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 983
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 984
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 985
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 986
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 987
ID ABO37663 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 988
ID ABM28427 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 989
ID ABM28732 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 990
ID ABM6376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 991
ID ABM7575 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 992
ID ABM34038 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 993
ID ABM34343 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 994
ID ABO20274 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 995
ID ABO21189 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 996
ID ABO22104 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 997
ID ABR96538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 998
ID ADA94289 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 999
ID ABR85716 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1000
ID ABR96968 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1001
ID ABM00554 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1002
ID ABM00249 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1003
ID ABO29681 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1004
ID ABM23547 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 1005
ID ABM29342 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1006
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1007
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1008
ID ABM20497 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1009
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1010
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1011
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1012
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1013
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1014
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1015
ID ABR81468 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1016
ID ABM77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1017
ID ABR89681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1018
ID ABM26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1019
ID ABR13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1020
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1021
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1022
ID ABM07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1023
ID ABM03909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1024
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1025
ID ABO41628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1026
ID ABO35223 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1027
ID ABM25072 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1028
ID ABO47464 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1029
ID ABO47769 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1030
ID ABO48379 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1031
ID ABO51429 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1032
ID ABO51734 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1033

ID ABO50514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1034
ID ABR79638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1035
ID ABM16900 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1036
ID ABO17932 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1037
ID ABO20884 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1038
ID ABR36843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1039
ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1040
ID ABM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1041
ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1042
ID ABM24157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1043
ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1044
ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1045
ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1046
ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1047
ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1048
ID AAM75453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1049
ID AAM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1050
ID AAM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1051
ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1052
ID ABO47098 standard; protein; 453 AA.

DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1053
ID ADA83153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1054
ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1055
ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1056
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1057
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1058
ID ABR84801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1059
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1060
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1061
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1062
ID ABR18120 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1063
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003052126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1064
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1065
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1066
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1067
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1068
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1069
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1070
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1071
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1072
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1073
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1074
ID ABM2952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1075
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1076
ID ABM1553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1077
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1078
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1079
ID ABO37968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1080
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1081
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1081
ID ABM6681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US200306868-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1082
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1083
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1084
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1085
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1086
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1087
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1088
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1089
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1090

ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1091
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1092
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1093
ID ABO05275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1094
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1095
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1096
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1097
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1098
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1099
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 1100
DE Human secreted standard; protein; 453 AA.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1101
ID ABR86021 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1102
ID ABM10673 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1103
ID ABM76672 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1104
ID ABR89376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1105
ID ABM12503 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1106
ID ABM05793 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1107
ID ABO34918 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1108
ID ABM02994 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1109
ID ABM18972 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1110
ID ABM19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1111
ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1112
ID ABO48989 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1113
ID ABR69032 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1114
ID ABR89071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1115
ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1116
ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1117
ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US200304921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1118
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1119
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1119
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1120
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1121
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1122
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1123
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1124
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1125
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1126
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1127
ID ABM1433 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 1128
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1129
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1130
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1131
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1132
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1133
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1134
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1135
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1136
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1137
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1138
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1139
ID ABM01774 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1140
ID ABM78197 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1141
ID ABR89986 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1142
ID ADA22196 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1143
ID ABM27512 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1144
ID ABM13113 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1145
ID ABO31816 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1146
ID ABM14028 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1147
ID ABM08233 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1148
ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1149
ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1150
ID ABM33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1151
ID ABM20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1152
ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1153
ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1154
ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1155
ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1156
ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1176
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1177
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1178
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1179
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1180
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1181
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1182
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1183
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1184
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1185

ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1186
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1187
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1188
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1189
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1190
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1191
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1192
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1193
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1194
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1195
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.

PN W0200306829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1196
ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1197
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1198
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1199
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1200
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1201
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1202
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1203
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1204
ID ADE26696 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1205
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1206
ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1207
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1208
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1209
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1210
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1211
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1212
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1213
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1214
ID ADI32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1215
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1216
ID ADE74221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1217
ID ADE74833 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1218
ID ADF35199 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1219
ID ADG11449 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1220
ID ADF96046 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1221
ID ADG04317 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1222
ID ADG00477 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1223
ID ADG87733 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1224
ID ADH26014 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068770-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1225
ID ADH19319 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1226
ID ADH32983 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1227
ID ADH20812 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1228
ID ADH19852 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1229
ID ADJ54722 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1230
ID ADJ64493 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1231
ID ADM31389 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1232
ID ADM36436 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 1233
ID ADM40241 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1234
ID ADN37849 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1235
ID AAY6647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 3; Length 455;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 1236
ID ADG10618 standard; protein; 472 AA.
DE Human STAT6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 7.0%; Score 85.5; DB 7; Length 472;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 1237
ID AAM41375 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 85.5; DB 4; Length 477;
Best Local Similarity 23.1%; Pred. No. 1.7;
RESULT 1238
ID AAG72466 standard; protein; 318 AA.
DE Human OR-1-like polypeptide query sequence, SEQ ID NO: 2147.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 7.0%; Score 85; DB 4; Length 318;
Best Local Similarity 19.5%; Pred. No. 1.1;
RESULT 1239
ID AAG71752 standard; protein; 318 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1433.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 7.0%; Score 85; DB 4; Length 318;
Best Local Similarity 19.5%; Pred. No. 1.1;
RESULT 1240
ID AAV31533 standard; protein; 450 AA.
DE Novel human secreted protein #2024.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 85; DB 4; Length 450;
Best Local Similarity 25.6%; Pred. No. 1.7;
RESULT 1241
ID AAY11065 standard; protein; 449 AA.
DE H. pylori ORF 09cpl0713_36359687_c1_119 inner membrane protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR) ASTRA AB.
Query Match 6.9%; Score 84; DB 2; Length 449;
Best Local Similarity 31.5%; Pred. No. 2.3;
RESULT 1242
ID ADO78101 standard; protein; 261 AA.
DE Human Claudin-18A2.1.
PN DE10254601-A1.
PD 03-JUN-2004.

PA (GANY-) GANYMED PHARM AG.
Query Match 6.9%; Score 83.5; DB 8; Length 261;
Best Local Similarity 25.6%; Pred. No. 1.2;
RESULT 1243
ID ADL95659 standard; protein; 316 AA.
DE Human novel GPCR1c.
PN US2003165829-A1.
PD 04-SEP-2003.
PA (PADJ/) PADJGARU M.
PA (MAJU/) MAJUMDER K.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (PERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (TCHS/) TCHERNEY V T.
PA (MISH/) MISHRA V.
PA (CASM/) CASMAN S.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
Query Match 6.9%; Score 83.5; DB 7; Length 316;
Best Local Similarity 22.1%; Pred. No. 1.6;
RESULT 1244
ID AAB90779 standard; protein; 180 AA.
DE Human shear stress-response protein SEQ ID NO: 58.
PN WO200125427-A1.
PD 12-APR-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJU/) NOJIMA H.
Query Match 6.8%; Score 82.5; DB 4; Length 180;
Best Local Similarity 27.4%; Pred. No. 0.93;
RESULT 1245
ID ADE83497 standard; protein; 180 AA.
DE Human protein P53801, SEQ ID NO 11093.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
Query Match 6.8%; Score 82.5; DB 7; Length 180;
Best Local Similarity 27.4%; Pred. No. 0.93;
RESULT 1246
ID AAB58380 standard; protein; 185 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 718.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.8%; Score 82.5; DB 3; Length 185;
Best Local Similarity 27.4%; Pred. No. 0.97;
RESULT 1247
ID AAB07073 standard; protein; 261 AA.
DE Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:90.
PN WO200154708-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 82.5; DB 4; Length 261;
Best Local Similarity 25.8%; Pred. No. 1.6;
RESULT 1248
ID ABG65079 standard; protein; 261 AA.
DE Human albumin fusion protein #1754.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 82.5; DB 5; Length 261;
Best Local Similarity 25.8%; Pred. No. 1.6;
RESULT 1249
ID ADL78346 standard; protein; 261 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1828.
PN US2004010134-A1.
PD 15-JUN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.8%; Score 82.5; DB 8; Length 261;
Best Local Similarity 25.8%; Pred. No. 1.6;

RESULT 1250
ID ADG42639 standard; protein; 867 AA.
DE Mouse prominin 1 precursor.
PN US2003204052-A1.
PD 30-OCT-2003.
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELI L.
PA (SHIM/) SHIMKETS R A.
Query Match
Best Local Similarity 25.0%; Score 82; DB 7; Length 867;
RESULT 1251
ID AAE07051 standard; protein; 261 AA.
DE Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:68.
PN WO200154708-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 261;
RESULT 1252
ID ABG5078 standard; protein; 261 AA.
DE Human albumin fusion protein #1753.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 5; Length 261;
RESULT 1253
ID ADL78345 standard; protein; 261 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1827.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 8; Length 261;
RESULT 1254
ID AAE07106 standard; protein; 276 AA.
DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:123.
PN WO200135708-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 276;
RESULT 1255
ID AAE10682 standard; protein; 316 AA.
DE G-protein coupled receptor 1c (GPCR1c).
PN WO200164879-A2.
PD 07-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 316;
RESULT 1256
ID AAE09449 standard; protein; 1694 AA.
DE Human sbg2487851a protein #2.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 1694;
RESULT 1257
ID AAE09448 standard; protein; 1709 AA.
DE Human sbg2487851a protein #1.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 1709;
RESULT 1258
ID ABG10466 standard; protein; 1839 AA.
DE Novel human diagnostic protein #10457.
PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.7%; Score 81.5; DB 4; Length 1839;
RESULT 1259
ID AAR13274 standard; protein; 254 AA.
DE Petunia extracellular chitinase.
PN EP440304-A.
PD 07-AUG-1991.
PA (MOGE-) MOGEN INT NV.
PA (UYLE-) RIKXSUNIV LEIDEN.
Query Match
Best Local Similarity 6.7%; Score 81; DB 2; Length 254;
RESULT 1260
ID AAM31296 standard; protein; 254 AA.
DE Petunia hybrida extracellular chitinase protein.
PN US5670706-A.
PD 23-SEP-1997.
PA (UYLE-) RIKXSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
Query Match
Best Local Similarity 6.7%; Score 81; DB 2; Length 254;
RESULT 1261
ID AAB07512 standard; protein; 254 AA.
DE Amino acid sequence of an extracellular chitinase.
PN US6087560-A.
PD 11-JUL-2000.
PA (UYLE-) RIKXSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
Query Match
Best Local Similarity 6.7%; Score 81; DB 3; Length 254;
RESULT 1262
ID AAY12855 standard; protein; 82 AA.
DE Human 5' EST secreted protein SEQ ID NO:445.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GESE-) GENSET.
Query Match
Best Local Similarity 6.6%; Score 80.5; DB 2; Length 82;
RESULT 1263
ID AAG71984 standard; protein; 320 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1665.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match
Best Local Similarity 6.6%; Score 80.5; DB 4; Length 320;
RESULT 1264
ID ABM69560 standard; protein; 157 AA.
DE Photorhabdus luminescens protein sequence #2657.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.6%; Score 80; DB 6; Length 157;
RESULT 1265
ID ABM70252 standard; protein; 391 AA.
DE Photorhabdus luminescens protein sequence #3349.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.5%; Score 79.5; DB 6; Length 391;
RESULT 1266
ID ABP8136 standard; protein; 430 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:2981.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.5%; Score 79.5; DB 5; Length 430;

Best Local Similarity 19.1%; Pred. No. 7.1;
 RESULT 1267
 ID ABB92528 standard; protein; 558 AA.
 DE Hericidially active polypeptide SEQ ID NO 1739.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match
 Best Local Similarity 22.7%; Pred. No. 10; Length 558;
 RESULT 1268
 ID ABB93024 standard; protein; 1143 AA.
 DE Hericidially active polypeptide SEQ ID NO 2235.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match
 Best Local Similarity 24.6%; Pred. No. 29; Length 1143;
 RESULT 1269
 ID ADA35359 standard; protein; 1160 AA.
 DE Acinetobacter baumannii protein #2700.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 22.8%; Pred. No. 29; Length 1160;
 RESULT 1270
 ID ADM04158 standard; protein; 144 AA.
 DE Human protein of the invention SEQ ID NO:2843.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match
 Best Local Similarity 27.8%; Pred. No. 1.7; Length 144;
 RESULT 1271
 ID ABP40601 standard; protein; 315 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5446.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 20.9%; Pred. No. 5.3; Length 315;
 RESULT 1272
 ID ABB40824 standard; protein; 502 AA.
 DE Protein encoded by Prokaryotic essential gene #26351.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 10; Length 502;
 RESULT 1273
 ID ABB68615 standard; protein; 546 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 32637.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match
 Best Local Similarity 20.9%; Pred. No. 11; Length 546;
 RESULT 1274
 ID ADF04297 standard; protein; 555 AA.
 DE Bacterial polypeptide #410.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 12; Length 555;
 RESULT 1275
 ID AAY41118 standard; protein; 667 AA.
 DE Rice sucrose transport protein (clone rlsc.pk0076.e2).
 PN WO9953068-A2.
 PD 21-OCT-1999.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 24.0%; Pred. No. 15; Length 667;

RESULT 1276
 ID AAM86525 standard; protein; 1305 AA.
 DE Adenyli cyclase type 9 protein amino acid sequence.
 PN WO9853856-A1.
 PD 03-DEC-1998.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match
 Best Local Similarity 23.5%; Pred. No. 39; Length 1305;
 RESULT 1277
 ID AAR9251 standard; protein; 1353 AA.
 DE Murine adenylylate cyclase 9.
 PN WO9625502-A1.
 PD 22-AUG-1996.
 PA (MEDT-) MEDICAL RES COUNCIL.
 Query Match
 Best Local Similarity 23.5%; Pred. No. 41; Length 1353;
 RESULT 1278
 ID ADE55614 standard; protein; 328 AA.
 DE Rat Protein CAA08796, SEQ ID NO 1433.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match
 Best Local Similarity 26.8%; Pred. No. 6.4; Length 323;
 RESULT 1279
 ID ADE55610 standard; protein; 328 AA.
 DE Rat Protein CAA08796, SEQ ID NO 1429.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match
 Best Local Similarity 26.8%; Pred. No. 6.4; Length 323;
 RESULT 1280
 ID ABB99400 standard; protein; 423 AA.
 DE Arabidopsis thaliana polypeptide SEQ ID NO 85.
 PN WO200266660-A2.
 PD 29-AUG-2002.
 PA (METN-) METANOMICS GMBH & CO KGAA.
 Query Match
 Best Local Similarity 20.7%; Pred. No. 9.1; Length 423;
 RESULT 1281
 ID ABB24464 standard; protein; 2005 AA.
 DE Novel human diagnostic protein #24455.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 24.7%; Pred. No. 83; Length 2005;
 RESULT 1282
 ID ABM72364 standard; protein; 309 AA.
 DE Staphylococcus aureus protein #1604.
 PN WO200294868-A2.
 PD 28-NOV-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match
 Best Local Similarity 20.8%; Pred. No. 6.7; Length 309;
 RESULT 1283
 ID ABU39954 standard; protein; 1059 AA.
 DE Protein encoded by Prokaryotic essential gene #25481.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 23.6%; Pred. No. 38; Length 1059;
 RESULT 1284
 ID AAU33615 standard; protein; 1062 AA.
 DE Pseudomonas aeruginosa cellular proliferation protein #59.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 23.6%; Pred. No. 38; Length 1062;

Best Local Similarity 24.5%; Pred. No. 38;
RESULT 1285
ID ABU15603 standard; protein; 1062 AA.
DE Protein encoded by Prokaryotic essential gene #1130.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 78; DB 6; Length 1062;
Best Local Similarity 24.5%; Pred. No. 38;
RESULT 1286
ID AB082891 standard; protein; 1065 AA.
DE Pseudomonas aeruginosa polypeptide #15066.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 78; DB 7; Length 1065;
Best Local Similarity 24.5%; Pred. No. 39;
RESULT 1287
ID ABO77741 standard; protein; 222 AA.
DE Pseudomonas aeruginosa polypeptide #9916.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 77.5; DB 7; Length 222;
Best Local Similarity 23.6%; Pred. No. 4.8;
RESULT 1288
ID ADM35793 standard; protein; 315 AA.
DE Human novel G protein-coupled receptor, GPCR1C.
PN US2003211485-A1.
PD 13-NOV-2003.
PA (GERL/) GERLACH V L.
PA (MACD/) MACDOUGALL J R.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (PADI/) PADIGARU M.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R A.
PA (TCHN/) TCHERNEV V T.
PA (MISH/) MISHRA V.
PA (CASM/) CASMAN S.
PA (SPYT/) SPYTEK K A.
PA (ZBRH/) ZERNHUSEN B.
Query Match 6.4%; Score 77.5; DB 7; Length 315;
Best Local Similarity 21.1%; Pred. No. 7.8;
RESULT 1289
ID AAY19919 standard; protein; 416 AA.
DE B. burgdorferi antigenic protein, t291.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 6.4%; Score 77.5; DB 2; Length 416;
Best Local Similarity 24.3%; Pred. No. 12;
RESULT 1290
ID ABU55897 standard; protein; 434 AA.
DE Protein encoded by Prokaryotic essential gene #11424.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77.5; DB 6; Length 434;
Best Local Similarity 20.8%; Pred. No. 12;
RESULT 1291
ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.4%; Score 77.5; DB 7; Length 453;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 1292
ID ABR62787 standard; protein; 459 AA.

DE MRSA hexose phosphate transporter SA214.
PN WO2003062466-A2.
PD 31-JUL-2003.
PA (UYBR-) UNIV BRISTOL.
Query Match 6.4%; Score 77.5; DB 7; Length 459;
Best Local Similarity 24.2%; Pred. No. 13;
RESULT 1293
ID ABU1896 standard; protein; 465 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 102.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.4%; Score 77.5; DB 6; Length 465;
Best Local Similarity 24.2%; Pred. No. 14;
RESULT 1294
ID ABW72036 standard; protein; 465 AA.
DE Staphylococcus aureus protein #1276.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77.5; DB 6; Length 465;
Best Local Similarity 24.2%; Pred. No. 14;
RESULT 1295
ID AAY19918 standard; protein; 500 AA.
DE B. burgdorferi antigenic protein, f291.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 6.4%; Score 77.5; DB 2; Length 500;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1296
ID AAU50487 standard; protein; 349 AA.
DE Propionibacterium acnes immunogenic protein #11383.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 77; DB 4; Length 349;
Best Local Similarity 27.4%; Pred. No. 10;
RESULT 1297
ID ABM47006 standard; protein; 349 AA.
DE Propionibacterium acnes transporter-related polypeptide #11682.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 77; DB 6; Length 349;
Best Local Similarity 27.4%; Pred. No. 10;
RESULT 1298
ID AAU55552 standard; protein; 1032 AA.
DE Haemophilus influenzae cellular proliferation protein #193.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 77; DB 4; Length 1032;
Best Local Similarity 22.6%; Pred. No. 48;
RESULT 1299
ID ABU30420 standard; protein; 1032 AA.
DE Protein encoded by Prokaryotic essential gene #15947.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 77; DB 6; Length 1032;
Best Local Similarity 22.6%; Pred. No. 48;
RESULT 1300
ID AAG30768 standard; protein; 1200 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36843.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 77; DB 3; Length 1200;
Best Local Similarity 28.4%; Pred. No. 60;
RESULT 1301
ID AAG30767 standard; protein; 1207 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36842.

EN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.3%; Score 77; DB 3; Length 1207;
RESULT 1302
ID AAG30766 standard; protein; 1215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36841.
EN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.3%; Score 77; DB 3; Length 1215;
RESULT 1303
ID ABB71131 standard; protein; 426 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40185.
EN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 4; Length 426;
RESULT 1304
ID ABB73387 standard; protein; 468 AA.
DE Candida albicans essential protein SEQ ID NO 7824.
PD 11-JUN-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 5; Length 468;
RESULT 1305
ID AAY41125 standard; protein; 563 AA.
DE Wheat sucrose transport protein (clone wlmk1.pk0002.e11).
EN WO9953068-A2.
PD 21-OCT-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 2; Length 563;
RESULT 1306
ID ABO66088 standard; protein; 614 AA.
DE Klebsiella pneumoniae polypeptide seqid 12605.
EN WO9610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 7; Length 614;
RESULT 1307
ID ABB71102 standard; protein; 1378 AA.
DE Murine homologue of attractin/mahogany (HAM) polypeptide.
EN WO200297120-A1.
PD 05-DEC-2002.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 6; Length 1378;
RESULT 1308
ID ABB98398 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Av1 gene cluster polypeptide frame 1.
EN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match
Best Local Similarity 6.3%; Score 76.5; DB 6; Length 19938;
RESULT 1309
ID AAM56388 standard; protein; 315 AA.
DE Fragment of the human GYT-2 transporter encoded by clone phg2-9b.
EN WO9807854-A1.
PD 26-FEB-1998.
PA (ALLX) ALLELIX NEUROSCIENCE INC.
Query Match
Best Local Similarity 6.3%; Score 76; DB 2; Length 315;
RESULT 1310
ID AAG81675 standard; protein; 337 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:444.
EN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAXO) GLAXO GROUP LTD.

Query Match
Best Local Similarity 6.3%; Score 76; DB 4; Length 337;
RESULT 1311
ID ABB48085 standard; protein; 431 AA.
DE Listeria monocytogenes protein #789.
EN WO20017335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 6.3%; Score 76; DB 5; Length 431;
RESULT 1312
ID ABB73417 standard; protein; 447 AA.
DE Staphylococcus aureus protein #2657.
EN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 6.3%; Score 76; DB 6; Length 447;
RESULT 1313
ID ABB10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
EN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.3%; Score 76; DB 4; Length 480;
RESULT 1314
ID ADF04316 standard; protein; 500 AA.
DE Bacterial polypeptide #429.
EN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.3%; Score 76; DB 7; Length 500;
RESULT 1315
ID AAB61263 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor.
EN WO200100810-A1.
PD 04-JUN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 6.3%; Score 76; DB 4; Length 631;
RESULT 1316
ID ABB19062 standard; protein; 643 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 339.
EN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match
Best Local Similarity 6.3%; Score 76; DB 6; Length 643;
RESULT 1317
ID ABB71337 standard; protein; 1079 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40803.
EN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.3%; Score 76; DB 4; Length 1079;
RESULT 1318
ID ABB10794 standard; protein; 93 AA.
DE Allolococcus oiticis antigenic protein SEQ ID NO:4266.
EN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match
Best Local Similarity 6.2%; Score 75.5; DB 6; Length 93;
RESULT 1319
ID ABB10762 standard; protein; 93 AA.
DE Allolococcus oiticis antigenic protein SEQ ID NO:4298.
EN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match
Best Local Similarity 6.2%; Score 75.5; DB 6; Length 93;

Best Local Similarity 31.4%; Pred. No. 2.4;
RESULT 1320
ID AD811392 standard; protein; 93 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:5668.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMPH) WYETH HOLDINGS CORP.
Query Match 6.2%; Score 75.5; DB 6; Length 93;
Best Local Similarity 31.4%; Pred. No. 2.4;
RESULT 1321
ID ABP63103 standard; protein; 397 AA.
DE FLO11 gene expression regulator At18.
PN WO200257456-A2.
PD 25-JUL-2002.
PA (MICR-) MICROBIA.
Query Match 6.2%; Score 75.5; DB 5; Length 397;
Best Local Similarity 26.3%; Pred. No. 19;
RESULT 1322
ID ABP35575 standard; protein; 397 AA.
DE Fungal ZBC protein sequence #1.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 6.2%; Score 75.5; DB 5; Length 397;
Best Local Similarity 26.3%; Pred. No. 19;
RESULT 1323
ID ABU9908 standard; protein; 409 AA.
DE Protein encoded by Prokaryotic essential gene #55435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 75.5; DB 6; Length 409;
Best Local Similarity 23.2%; Pred. No. 19;
RESULT 1324
ID ADN73661 standard; protein; 476 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants Segid 1556.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match 6.2%; Score 75.5; DB 8; Length 476;
Best Local Similarity 21.5%; Pred. No. 24;
RESULT 1325
ID ADA36649 standard; protein; 277 AA.
DE Acinetobacter baumannii protein #3810.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 75; DB 6; Length 277;
Best Local Similarity 39.2%; Pred. No. 13;
RESULT 1326
ID ABB98338 standard; protein; 292 AA.
DE Human anti-tenascin C monoclonal antibody SEQ ID NO 2.
PN JP2002234900-A.
PD 23-AUG-2002.
PA (MIED-) MIE DAIGAKUCHO.
Query Match 6.2%; Score 75; DB 6; Length 292;
Best Local Similarity 34.7%; Pred. No. 14;
RESULT 1327
ID ADP04284 standard; protein; 292 AA.
DE Human tenascin C fibronectin III-like domain BCD domain polypeptide.
PN JP2004138489-A.
PD 13-MAY-2004.
PA (WENE-) WENEKI SEIBUTSU KENKYUSHO KK.
Query Match 6.2%; Score 75; DB 8; Length 292;
Best Local Similarity 34.7%; Pred. No. 14;
RESULT 1328
ID ABU29147 standard; protein; 527 AA.
DE Protein encoded by Prokaryotic essential gene #14674.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 75; DB 6; Length 527;

Best Local Similarity 21.2%; Pred. No. 32;
RESULT 1329
ID ADN05803 standard; protein; 2000 AA.
DE Antipeptidic protein sequence #1065.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTH) GENENTECH INC.
Query Match 6.2%; Score 75; DB 8; Length 2000;
Best Local Similarity 34.7%; Pred. No. 2.1e+02;
RESULT 1330
ID ABO01379 standard; protein; 2108 AA.
DE Human protein NOV35b.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.2%; Score 75; DB 6; Length 2108;
Best Local Similarity 34.7%; Pred. No. 2.3e+02;
RESULT 1331
ID ADN96130 standard; protein; 2108 AA.
DE Human NOVX polypeptide #92.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LIL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PAT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MAL/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLER I.
PA (MACD/) MACDOUGALL J R.
PA (ELIE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 6.2%; Score 75; DB 8; Length 2108;
Best Local Similarity 34.7%; Pred. No. 2.3e+02;
RESULT 1332
ID AAO30847 standard; protein; 2110 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.2%; Score 75; DB 7; Length 2110;
Best Local Similarity 34.7%; Pred. No. 2.3e+02;
RESULT 1333
ID ADM80773 standard; protein; 2110 AA.
DE Human CADECM-2 protein SEQ ID NO:2.
PN WO2004015396-A2.

PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 34.7%; Score 75; DB 8; Length 2110;
RESULT 1334
ID AAG70361 standard; protein; 2167 AA.
DE Novel human thrombopoietin variant protein, NV-20.
PN US2002068342-A1.
PD 06-JUN-2002.
PA (KHOS/) KHOSRAVI R.
PA (BERN/) BERNSTEIN J.
Query Match
Best Local Similarity 34.7%; Score 75; DB 5; Length 2167;
RESULT 1335
ID AAR94562 standard; protein; 2199 AA.
DE Human cytotoxicin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCTR) SCRIPPS RES INST.
Query Match
Best Local Similarity 34.7%; Score 75; DB 2; Length 2199;
RESULT 1336
ID ABO01378 standard; protein; 2199 AA.
DE Human Protein NOV35a.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 34.7%; Score 75; DB 6; Length 2199;
RESULT 1337
ID ADN96128 standard; protein; 2199 AA.
DE Human NOVA polypeptide #91.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LITL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATY/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match
Best Local Similarity 34.7%; Score 75; DB 8; Length 2199;
RESULT 1338

RESULT 1338
ID AAB36935 standard; protein; 2201 AA.
DE Human tenascin-C.
PN WO200066628-A1.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match
Best Local Similarity 34.7%; Score 75; DB 4; Length 2201;
RESULT 1339
ID ABP97745 standard; protein; 2201 AA.
DE Amino acid sequence of human HXB polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match
Best Local Similarity 34.7%; Score 75; DB 6; Length 2201;
RESULT 1340
ID AAM78955 standard; protein; 2201 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.
PD 12-SEP-2003.
PA (GEOU-) UNIV GEORGETOWN.
Query Match
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;
RESULT 1341
ID ADD69400 standard; protein; 2201 AA.
DE Human tenascin protein - SEQ ID 136.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEEC INC.
Query Match
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;
RESULT 1342
ID ADD47935 standard; protein; 2201 AA.
DE Human Protein XP_005348, SEQ ID NO 13631.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;
RESULT 1343
ID ADE62224 standard; protein; 2201 AA.
DE Human Protein P24821, SEQ ID NO 8153.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;
RESULT 1344
ID ADO17766 standard; protein; 2201 AA.
DE Differentially expressed protein lvi, SEQ ID 1.
PN WO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 34.7%; Score 75; DB 8; Length 2201;
RESULT 1345
ID ADQ19756 standard; protein; 2201 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 34.7%; Score 75; DB 8; Length 2201;
RESULT 1346
ID AAM41065 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5996.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 34.7%; Score 74.5; DB 4; Length 210;

Best Local Similarity 22.8%; Pred. No. 9.9;
RESULT 1347
ID AAM41066 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5997.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74.5; DB 4; Length 210;
Best Local Similarity 22.8%; Pred. No. 9.9;
RESULT 1348
ID AAM41067 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5998.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74.5; DB 4; Length 210;
Best Local Similarity 22.8%; Pred. No. 9.9;
RESULT 1349
ID AAB46359 standard; protein; 255 AA.
DE H. pylori HPC104 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 6.1%; Score 74.5; DB 4; Length 255;
Best Local Similarity 18.6%; Pred. No. 13;
RESULT 1350
ID ABP58049 standard; protein; 289 AA.
DE Saccharomyces cerevisiae aquaporin.
PN WO200290557-A2.
PD 14-NOV-2002.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.1%; Score 74.5; DB 6; Length 289;
Best Local Similarity 26.8%; Pred. No. 16;
RESULT 1351
ID AAB78974 standard; protein; 364 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:208.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.1%; Score 74.5; DB 4; Length 364;
Best Local Similarity 20.3%; Pred. No. 21;
RESULT 1352
ID AAG92975 standard; protein; 378 AA.
DE C glutamicum protein fragment SEQ ID NO: 6729.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOM) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 74.5; DB 4; Length 378;
Best Local Similarity 20.3%; Pred. No. 23;
RESULT 1353
ID AAB78973 standard; protein; 412 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:206.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.1%; Score 74.5; DB 4; Length 412;
Best Local Similarity 20.3%; Pred. No. 26;
RESULT 1354
ID ABU49116 standard; protein; 468 AA.
DE Protein encoded by Prokaryotic essential gene #34643.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 74.5; DB 6; Length 468;
Best Local Similarity 25.7%; Pred. No. 31;
RESULT 1355
ID ABB60065 standard; protein; 473 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6987.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 74.5; DB 4; Length 473;

Best Local Similarity 16.5%; Pred. No. 31;
RESULT 1356
ID AAN18057 standard; protein; 524 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 202.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 524;
Best Local Similarity 22.2%; Pred. No. 36;
RESULT 1357
ID ABB10423 standard; protein; 524 AA.
DE Human CDNA SEQ ID NO: 731.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 524;
Best Local Similarity 22.2%; Pred. No. 36;
RESULT 1358
ID ABP67010 standard; protein; 524 AA.
DE Human polypeptide SEQ ID NO 731.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.1%; Score 74.5; DB 5; Length 524;
Best Local Similarity 22.2%; Pred. No. 36;
RESULT 1359
ID ADB31681 standard; protein; 524 AA.
DE Human novel protein SEQ ID NO 202.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 7; Length 524;
Best Local Similarity 22.2%; Pred. No. 36;
RESULT 1360
ID ABU20338 standard; protein; 541 AA.
DE Protein encoded by Prokaryotic essential gene #5865.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 74.5; DB 6; Length 541;
Best Local Similarity 20.3%; Pred. No. 38;
RESULT 1361
ID ABB90801 standard; protein; 618 AA.
DE Hericidially active polypeptide SEQ ID NO 12.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (PARB) BAYER AG.
Query Match 6.1%; Score 74.5; DB 5; Length 618;
Best Local Similarity 27.7%; Pred. No. 46;
RESULT 1362
ID ADN74317 standard; protein; 618 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 2212.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPDESIGN NV.
Query Match 6.1%; Score 74.5; DB 8; Length 618;
Best Local Similarity 27.7%; Pred. No. 46;
RESULT 1363
ID ABB10186 standard; protein; 654 AA.
DE Human CDNA SEQ ID NO: 494.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 654;
Best Local Similarity 22.2%; Pred. No. 49;
RESULT 1364
ID ABP6773 standard; protein; 654 AA.
DE Human polypeptide SEQ ID NO 494.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 22.2%; Pred. No. 49; Length 654;
RESULT 1365
ID ADP04132 standard; protein; 705 AA.
DE Human colon specific protein SEQ ID NO:113.
PN W02004050858-A2.
PD 17-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 55; Length 705;
RESULT 1366
ID AAG38915 standard; protein; 1030 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48077.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 27.7%; Pred. No. 94; Length 1030;
RESULT 1367
ID AAG38914 standard; protein; 1133 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48076.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 27.7%; Pred. No. 1.1e+02; Length 1133;
RESULT 1368
ID AAG38913 standard; protein; 1193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48075.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 27.7%; Pred. No. 1.2e+02; Length 1193;
RESULT 1369
ID ABU79090 standard; protein; 1709 AA.
DE Human sialic acid binding Ig-superfamily lectin, siglec-1.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;
RESULT 1370
ID ADP4331 standard; protein; 1709 AA.
DE Superantigen associated protein seq id 51.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;
RESULT 1371
ID ADJ69756 standard; protein; 1709 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1562.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;
RESULT 1372
ID ADH71514 standard; protein; 1709 AA.
DE Human protein of the invention NOV14g SEQ ID NO:410.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;
RESULT 1373
ID ABG01737 standard; protein; 161 AA.
DE Novel human diagnostic protein #1728.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSQ INC.
Query Match
6.1%; Score 74; DB 5; Length 161;

Best Local Similarity 30.0%; Pred. No. 7.7;
RESULT 1374
ID AAB92492 standard; protein; 448 AA.
DE Human protein sequence SEQ ID NO:10589.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 23.5%; Pred. No. 33; Length 448;
RESULT 1375
ID ABB97449 standard; protein; 448 AA.
DE Novel human protein SEQ ID NO: 717.
PN W0200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSQ INC.
Query Match
Best Local Similarity 23.5%; Pred. No. 33; Length 448;
RESULT 1376
ID ABB82639 standard; protein; 448 AA.
DE Human hypothetical protein FLJ10060.
PN W0200286060-A2.
PD 31-OCT-2002.
PA (IMME-) IMMERGE BIOTHERAPEUTICS INC.
Query Match
Best Local Similarity 23.5%; Pred. No. 33; Length 448;
RESULT 1377
ID ABB92535 standard; protein; 555 AA.
DE Herbicidally active polypeptide SEQ ID NO 1746.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 26.4%; Pred. No. 45; Length 555;
RESULT 1378
ID ADG42638 standard; protein; 857 AA.
DE Rat prolamin.
PN US2003204052-A1.
PD 30-OCT-2003.
PA (HERR/) HERPMANN J L.
PA (RAST/) RASTELT L.
PA (SHIM/) SHIMKETS R A.
Query Match
Best Local Similarity 23.0%; Pred. No. 83; Length 857;
RESULT 1379
ID AAB40566 standard; protein; 261 AA.
DE Human ORFX ORF330 polypeptide sequence SEQ ID NO:660.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1380
ID AAY70675 standard; protein; 261 AA.
DE Human stomach protein zsig28.
PN W0200015659-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1381
ID AAY92235 standard; protein; 261 AA.
DE Claudin homologue from clone 324646 cDNA.
PN W0200020447-A2.
PD 13-APR-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1382
ID AAY94433 standard; protein; 261 AA.
DE Human PRO1572 (UNQ778) amino acid sequence SEQ ID NO:326.
PN W0200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1383
ID AAB6181 standard; protein; 261 AA.
DE Protein of the invention #93.
PN WO20078961-A1.
PD 28-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1384
ID AAU9201 standard; protein; 261 AA.
DE Human PRO polypeptide sequence #178.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1385
ID AAB87584 standard; protein; 261 AA.
DE Human PRO1572.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1386
ID ABG60912 standard; protein; 261 AA.
DE Protein encoded by lung specific gene #2.
PN WO200218576-A2.
PD 07-MAR-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1387
ID ABG5909 standard; protein; 261 AA.
DE Human secreted/transmembrane protein PRO1572.
PN US200219130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1388
ID ABUS857 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1389
ID ABUS8125 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US200302127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1390
ID ABUS8440 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1391
ID ABR66314 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1392
ID ABR65704 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1393
ID ABUS9644 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1394
ID ABUS8283 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1395
ID ABUS9004 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1396
ID ABR68253 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1397
ID ABUS6306 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1398
ID ABUS92737 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1399
ID ABO08814 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1400
ID ABO02866 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1401
ID ABR75020 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1402
ID ABR94782 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1403
ID ABR94782 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003044926-A1.
PD 06-MAR-2003.
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PD Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1403
ID AB085755 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1404
ID AB098915 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003031353-A1.
PD 16-JAN-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1405
ID AB098130 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1406
ID AB091836 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1407
ID AB089529 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1408
ID AB086370 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1409
ID AB067583 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1410
ID AB080611 standard; protein; 261 AA.
DE Human PRO protein #178.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1411
ID AB090934 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1412
ID AB033993 standard; protein; 261 AA.
DE Human secreted/transmembrane protein PRO1572.
PN US2003009013-A1.
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PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1413
ID ABR9529 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1414
ID ABR98919 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1415
ID AB016442 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1416
ID ABR92342 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1417
ID AB018983 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1418
ID ABR78404 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1419
ID AB072010 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1420
ID AB055140 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1421
ID AB000279 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
RESULT 1422
ID AB011611 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036124-A1.
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RESULT 1463
ID ABR65031 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1464
ID ABO27339 standard; protein; 261 AA.
DE Human secreted/transmembrane polypeptide PRO1572.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1465
ID ABR6863 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1466
ID ABO0679 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1467
ID ABR99224 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1468
ID ABU57108 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1469
ID ABU660 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1470
ID ABU82347 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1471
ID ABU87358 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1472
ID ABU83830 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1473
ID ABO08204 standard; protein; 261 AA.

DE Human PRO polypeptide #178.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1474
ID ABU92534 standard; protein; 261 AA.
DE Human secreted/transmembrane protein PRO1572.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1475
ID ABU81915 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1476
ID ABU66079 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1477
ID ABU81204 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1478
ID ABR59908 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1479
ID ABU94096 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1480
ID ABU99949 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1481
ID ABR66619 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1482
ID ABR91037 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Pred. No. 18; Length 261;
RESULT 1483
ID ABO53318 standard; protein; 261 AA.

DE Novel human secreted and transmembrane protein PRO1572.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB094464 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB079346 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB086675 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB086980 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB094769 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB004696 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABR70445 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB098610 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABR66009 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABR64726 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.

PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABR79651 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB093042 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB096001 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB091221 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID AB090314 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABO09729 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;
ID ABO11001 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 18;